

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 22, 2004, 05:19:48 ; Search time 391 Seconds  
(without alignments)

2238.181 Million cell updates/sec

Title: US-09-935-390A-23

Perfect score: 1167  
Sequence: 1 MERRHPVCSGTQPTQFRCS.....TVSTTDETHLVNHTIRPL 206

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 5747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-Q/cn2\_1/USPTO\_spool/US09935390/runat 20042004.144849.10373/app query.fasta.1.391  
-DB=N Geneseq 29Jan04 -QFMT=fastap -SUFFIX=ing -MINMATCH=0.1 -LOCPCL=0  
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09935390 @CGN\_1\_1\_470 @runat 20042004.144849.10373 -NCPUP=6 -ICPU=3  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 29Jan04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1167	100.0	1505	2 AAV43604	AAV43604 Human sec
2	1167	100.0	1542	2 AAT90038	Aat90038 Hepatocyt
3	1167	100.0	1542	2 AAX02200	Aax02200 Human HAI
4	1167	100.0	1870	3 AAL46725	Aal46725 Human pro
5	1163	99.7	2482	2 AAF30055	Aaf30055 Human CDN
6	1163	99.7	2482	4 RAD16721	Rad16721 Human hep
7	1163	99.7	2482	6 ABK40259	Abk40259 cDNA enco
8	1163	99.7	2482	6 ABL88092	AbL88092 Human PRO

9	1163	99.7	2482	6 ABK69965	AbK69965 cDNA enco
10	1163	99.7	2482	6 ABL95581	AbL95581 Human ang
11	1163	99.7	2482	8 ADA01277	Ada01277 Human PRO
12	1163	99.7	2482	8 ADA43706	Ada43706 Human CDN
13	1163	99.7	2482	8 ADA43474	Ada43474 Human CDN
14	1163	99.7	2482	8 ADA01149	Ada01149 Human PRO
15	1163	99.7	2482	8 ADA01033	Ada01033 Human CDN
16	1163	99.7	2482	8 ADA43590	Ada43590 Human CDN
17	1163	99.7	2482	8 ADA06852	Ada06852 Human PRO
18	1163	99.7	2482	8 ADA08340	Ada08340 Novel hum
19	1163	99.7	2482	8 ADB99633	AdB99633 Human PRO
20	1163	99.7	2482	8 ADB86916	AdB86916 Human PRO
21	1163	99.7	2482	8 ADB66071	AdB66071 Human CDN
22	1163	99.7	2482	8 ADB99749	AdB99749 Human PRO
23	1163	99.7	2482	9 ADB99404	AdB99404 Novel hum
24	1163	99.7	2482	9 ADB65955	AdB65955 Human CDN
25	1163	99.7	2482	9 ADC23353	AdC23353 Human CDN
26	1163	99.7	2482	9 ADC26046	AdC26046 Human PRO
27	1163	99.7	2482	9 ADD10330	AdD10330 Human sec
28	1163	99.7	2482	9 ADD11290	AdD11290 Human sec
29	1163	99.7	2482	9 ADD37083	AdD37083 Human sec
30	1163	99.7	2482	9 ADE04873	AdE04873 Human PRO
31	1163	99.7	2482	9 ADE11179	AdE11179 Human PRO
32	1163	99.7	2482	9 ADD88110	AdD88110 Human PRO
33	1163	99.7	2482	9 ADD95405	AdD95405 Human CDN
34	1163	99.7	2482	9 ADE06335	AdE06335 Human PRO
35	1163	99.7	2482	9 ADE38110	AdE38110 Human PRO
36	1163	99.7	2482	9 ADD88226	AdD88226 Human PRO
37	1163	99.7	2482	9 ADD90807	AdD90807 Human CDN
38	1163	99.7	2482	10 ADE51660	AdE51660 Human CDN
39	1163	99.7	2482	10 ADE51776	AdE51776 Human CDN
40	1163	99.7	2482	10 ADE37634	AdE37634 Human CDN
41	1163	99.7	2482	10 ADE37518	AdE37518 Human CDN
42	1163	99.7	2482	10 ADD95289	AdD95289 Human CDN
43	1163	99.7	2482	10 ADE37989	AdE37989 Human PRO
44	1163	99.7	2482	10 ADE76078	AdE76078 Human PRO
45	1163	99.7	2482	10 ADE39401	AdE39401 Human PRO

#### ALIGNMENTS

RESULT 1  
AAV43604  
ID AAV43604 standard; DNA; 1505 BP.

XX AC AAV43604;

XX DT 24-SEP-1998 (first entry)

XX DE Human secreted protein 4 encoding DNA.

XX KW Secreted protein; human; cell proliferation; cytokine activity;  
XX KW tissue growth; cellular differentiation; regeneration; activin;  
XX KW chemotactic; haemostatic; thrombolytic; tumour inhibition;  
XX KW anti-inflammatory activity; biomarker; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 171..791

FT /\*tag= a

FT /product= "human secreted protein"

XX PN WO9825959-A2.

XX PD 18-JUN-1998.

XX PF 11-DEC-1997; 97WO-US022787.

XX PR 11-DEC-1996; 96US-0032757P.

XX PA (CHIR ) CHIRON CORP.

XX

PI Escobedo J, Hu Q, Garcia P, Williams LT, Kothakota S;  
 XX MPI: 1998-348453/30.  
 DR P-FSDB; AAW63684.

Secreted human polypeptides - having cytokine, cell proliferation or  
 PT differentiation, activin or inhibin, tumour inhibition or anti-  
 PT inflammatory activities.

XX Claim 6; Page 31-32; 78pp; English.

XX This DNA encodes a human secreted protein. The specification provides  
 CC secreted protein sequences (AAW63681 to AAW63699) encoded by the nucleic  
 CC acid sequences shown in AAW43601 to AAW43619. The invention provides a  
 CC method of identifying a secreted polypeptide which is modified by rough  
 CC microsomes. The secreted proteins can be used in assays to determine  
 CC biological activities, such as cytokine, cell proliferation, or cellular  
 CC differentiation activities, tissue growth or regeneration, activin or  
 CC inhibin activity, chemotactic or chemokinetic activity, haemostatic or  
 CC thrombolytic activity, receptor/ligand activity, tumour inhibition, or  
 CC anti-inflammatory activity. The proteins can also be used as biomarkers,  
 CC to identify tissues or cell types which express the proteins, or a stage-  
 CC or disease-specific alteration in protein expression. They can be used in  
 CC protein interaction assays, to identify ligands or binding proteins.  
 CC Compounds which affect the biological activities of the secreted proteins  
 CC or their ability to interact with specific ligands can be identified  
 CC using the proteins in screening assays. The proteins and antibodies that  
 CC bind specifically to the protein can also be used to design diagnostic  
 CC tests and therapeutic compositions for diseases which may be associated  
 CC with altered expression of these proteins. Fusion proteins comprising,  
 CC e.g. signal sequences or transmembrane domains of the proteins can be  
 CC used to target other protein domains to cellular membrane or they can be  
 CC secreted extracellularly

XX SQ Sequence 1505 BP; 332 A; 450 C; 406 G; 317 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 7,51e-115 Length: 1505  
 Score: 1167.00 Matches: 206  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-09-935-390A-23 (1-206) x AAW43604 (1-1505)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
 Db 171 ATGGAAGGCGCATCCAGTGTGCTCTGGCACTGTGAGCCACCCAGTTCGGCTGCAGC 230  
 QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40  
 Db 231 AATGGCTGTGCAATGACAGTTCCTGGAGTGTGACGACACCCCACTGCCCCGACGCC 290  
 QY 41 SerAspGluAlaAlaCysGluIleValThrSerGlyPheAspGluLeuGlnArgIleHis 60  
 Db 291 TCCGACGAGCTGCTGTGAAATACACAGATGGCTTTGACGAGCTCCAGCGCATCCAT 350  
 QY 61 PheProSerAspIleGlyHisCysValAspLeuProAspThrGlyLeuCysIleGluSer 80  
 Db 351 TTCCCCAGCGCAACAGGCGACTCGGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 410  
 QY 81 IleProArgTyrTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100  
 Db 411 ATCCCGGCTGTGTACTACACCCCTTCAGCAACACTGGCGCCGCTTACCTATGGTGGT 470  
 QY 101 CysTyrGlyAsnIleAsnAsnGluGluGluGlnGlnCysLeuGluSerCysArgGly 120  
 Db 471 TGTACGGCAACAAGAACCACTTGGAGGAAGAGCAGCAGTGTGCTGAGTCTTGTGCGGCG 530  
 QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140  
 Db 531 ATCTCCAGAGATGTGTTTGGCTGTGAGCGGGAATCCCATTTCCAGCAGCAGGCTCT 590

QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeu 160  
 Db 591 GTGGAGATGGCTGTCCAGTGTTCCTGGTCACTGTCATGTGGTGTGGTAGGCACTTG 650  
 QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180  
 Db 651 GGTACTGCTTCTTCAAGAACACAGAGAAAGGACTTCCACGACACACCCACCCACCA 710  
 QY 181 ProThrProAlaSerSerThrValSerThrGluAspThrGluHisLeuValTyrAsn 200  
 Db 711 CCACACCCCTGCGAGCTCCACTGTCTCCACTACGAGACACGAGGACCTTGGTCTATAAC 770  
 QY 201 HisThrThrArgProLeu 206  
 Db 771 CACACCAACGCGGCCCTC 788

## RESULT 2

AAAT90038  
 ID AAT90038 standard; cDNA to mRNA; 1542 BP.

AC AAT90038;

DT 21-NOV-1997 (first entry)

XX Hepatocyte growth factor activator inhibitor cDNA.

XX Inhibition; inhibitor; protease; hepatocyte; growth factor; activation;  
 KW activator; human; cancer; cell line; MKN45; regulation; regulator;  
 KW antibody; kinetic study; assay standard; ds.

OS Homo sapiens.

Key	Location/Qualifiers
CDS	1..1542
sig_peptide	/tag= a
mat_peptide	1..105
	/tag= b
	109..1539
	/tag= c
	/product= "HGFA_inhibitor"

PN BP759467-A2.

PD 26-FEB-1997.

PP 23-JUL-1996; 96EP-00111870.

PR 24-JUL-1995; 95JP-00187135.

PA (MITU) MITSUBISHI CHEM CORP.

PI Shimomura T, Kawaguchi T, Kitamura N, Miyazawa K;

DR MPI; 1997-147516/14.

DR P-FSDB; AAW27368.

PT New hepatocyte growth factor activator inhibitor and DNA - regulates  
 PT hepatocyte growth factor and/or HGF activator in vivo or in vitro, and  
 PT are used in kinetic studies.

PS Claim 10; Page 28-30; 38pp; English.

XX The present sequence encodes an inhibitor of the protease activity of  
 CC hepatocyte growth factor (HGF) activator (HGFA), which has a molecular  
 CC weight of about 40 kD when determined by SDS-PAGE. The inhibitor, which  
 CC was isolated from the human cancer cell line MKN45, can be used as an in  
 CC vivo or in vitro regulatory factor for HGF or HGFA. It can also be used  
 CC to raise antibodies, useful in kinetic studies of the inhibitor, or as  
 CC assay standards

SQ Sequence 1542 BP; 319 A; 507 C; 439 G; 277 T; 0 U; 0 Other;

Alignment Scores: 7.76e-115 Length: 1542  
Score: 1167.00 Matches: 206  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-09-935-390A-23 (1-206) x AAX02200 (1-1542)

QY 1 MetGluArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
DB 922 ATGGAAGGGCGGCTCAGTGTCTCTGGACCTGTGAGGACCTCTGCAAGGAGGC 981

QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40  
DB 982 AATGGCTGTCTGATCGACAGTTTCTGGAGTGTGACACACCCCACTGCCCCGAGGC 1041

QY 41 SerAspGluAlaCysGluLysTyrrSerGlyPheAspGluLeuGlnArgIleHis 60  
DB 1042 TCCGACGAGGCTGCTGTGAAATAACAGAGTGGCTTTGACGAGCTCCAGGCGATCAT 1101

QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
DB 1102 TTCCCAAGTGACAAAGGGGACTCGGTGGACCTGCGCAGACACAGGACTCTGCAAGGAGGC 1161

QY 81 IleProArgTrpTyrrAsnProPheSerGluHisCysAlaArgPheThrTyrrGlyGly 100  
DB 1162 ATCCCGCGCTGTACTACAAACCTTTACAGGAACTGCGCCGCTTACCTATGCTGGT 1221

QY 101 CysTyrrGlyAsnLysAsnAsnPhedGluGluGlnGlnCysLeuGluSerCysArgGly 120  
DB 1222 TGTATGGCAACAGAACACTTTGAGGAAGAGCAGTGTGCTGAGTCTTTGTCGCGC 1281

QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140  
DB 1282 ATCTCCAGAGAGTGTGTGGCTGAGCGGGAATCCCTATCCAGCACAGGCTCT 1341

QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160  
DB 1342 GTGGAGATGGCTGTGCGAGTGTCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCT 1401

QY 161 GlyTyrrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180  
DB 1402 GGTACTGCTCTTCAAGAACAGAGAGGAGTCTTCCAGGACACACACACACACCA 1461

QY 181 ProThrProAlaSerThrValSerThrThrThrThrThrThrThrThrThrThrThr 200  
DB 1462 CCCACCCCTGCGAGCTCCACTGTCTCCACTCCGAGGACAGGAGCAGCTGCTATAC 1521

QY 201 HisThrThrArgProLeu 206  
DB 1522 CACACCCCGGCCCCC 1539

RESULT 3  
AAX02200  
ID AAX02200 standard; DNA; 1542 BP.  
XX AC AAX02200;  
XX AC AAX02200;  
DT 30-APR-1999 (first entry)  
XX DE Human HAI-1 cDNA.  
XX Hepatocyte growth factor; HAI-1; HGF inhibiting factor; human; plasmin;  
XX treatment; prevention; protease activity; plasma; urokinase; trypsin; ss.  
OS Homo sapiens.  
XX Key Location/Qualifiers  
XX CDS 1..1542  
XX /tag= a  
XX /product= "HAI-1"

sig\_peptide 1..105  
mat\_peptide /tag= b  
106..1539  
/tag= c  
JP11035480-A.  
09-FEB-1999.  
15-JUL-1997; 97JP-00189480.  
15-JUL-1997; 97JP-00189480.  
(MITU) MITSUBISHI CHEM CORP.  
WPI; 1999-186215/16.  
P-PSDB; AAW92653.  
A preventive and/or treating agent for the diseases caused by the  
exasperation of activity of protease - inhibits protease activity of  
hepatocyte growth factor (HGF) activator.  
Claim 7; Page 6-8; 8pp; Japanese.  
This invention describes a preventive and/or treating agent for the  
diseases caused by the exasperation of activity of protease of plasma  
kallikrein, plasmin, urokinase and trypsin. The agent contains a protein,  
HAI-1 which has the following properties, M.W. of ca. 40,000 to 57,000  
Dalton by SDS-PAGE and an activity of inhibiting protease activity of  
hepatocyte growth factor (HGF) activator. The HGF inhibiting activity of  
the protein is specific. HAI-1 shows a high inhibiting activity on  
plasmin, trypsin, HGF activator and plasma kallikrein but substantially  
no inhibiting activity on thrombin. This sequence encodes the human HAI-1  
protein  
Sequence 1542 BP; 319 A; 507 C; 439 G; 277 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 7.76e-115 Length: 1542  
Score: 1167.00 Matches: 206  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-09-935-390A-23 (1-206) x AAX02200 (1-1542)

QY 1 MetGluArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
DB 922 ATGGAAGGGCGGCTCAGTGTCTCTGGACCTGTGAGGACCTCTGCAAGGAGGC 981

QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40  
DB 982 AATGGCTGTCTGATCGACAGTTTCTGGAGTGTGACACACCCCACTGCCCCGAGGC 1041

QY 41 SerAspGluAlaCysGluLysTyrrSerGlyPheAspGluLeuGlnArgIleHis 60  
DB 1042 TCCGACGAGGCTGCTGTGAAATAACAGAGTGGCTTTGACGAGCTCCAGGCGATCAT 1101

QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
DB 1102 TTCCCAAGTGACAAAGGGGACTCGGTGGACCTGCGCAGACACAGGACTCTGCAAGGAGGC 1161

QY 81 IleProArgTrpTyrrAsnProPheSerGluHisCysAlaArgPheThrTyrrGlyGly 100  
DB 1162 ATCCCGCGCTGTACTACAAACCTTTACAGGAACTGCGCCGCTTACCTATGCTGGT 1221

QY 101 CysTyrrGlyAsnLysAsnAsnPhedGluGluGlnGlnCysLeuGluSerCysArgGly 120  
DB 1222 TGTATGGCAACAGAACACTTTGAGGAAGAGCAGTGTGCTGAGTCTTTGTCGCGC 1281

QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140





# RESULT 5 AAF30055

ID AAF30055 standard; cDNA; 2482 BP.  
XX AC AAF30055;

DT 30-APR-2001 (first entry)

DE Human cDNA encoding PRO256.

XX PRO256; UNQ223; human; immune disease; autoimmune disease; antirheumatic;  
XX antiarthritic; antiinflammatory; antianaemic; immunosuppressive;  
XX antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide;  
XX dermatological; antipsoriatic; antiallergic;  
XX immunostimulant; protease inhibitor; ss.

XX Homo sapiens.

XX Key location/Qualifiers

FT CDS 188..1777

FT /\*tag= a

FT sig\_peptide 188..292

FT /\*tag= b

FT mat\_peptide 293..1774

FT /\*tag= c

XX WO200105972-A1.

XX 25-JAN-2001.

XX 15-MAR-2000; 2000WO-US006884.

XX 20-JUL-1999; 99US-0144758P.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ;

XX Gurney AL, Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D;

XX Watanabe CK, Wood WI;

XX WPI; 2001-103149/11.

XX P-PSDB; AAB20113.

XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for

XX diagnosing and treating immune-related disorders, such as multiple

XX sclerosis, rheumatoid arthritis and diabetes.

XX Claim 21; Fig 11; 127pp; English.

XX The present sequence is that of cDNA clone DNA35880-1160 (ATCC 209379)  
XX encoding novel human immunomodulator protein PRO256 (UNQ223) (see  
XX AAB20113). The clone was isolated from a human placenta cDNA library. The  
XX predicted protein (58 kDa, pI 6.22) shows homology to human bikunin,  
XX indicating protease inhibitor activity. The invention provides  
XX polynucleotides (see AAF30050-62) encoding novel human PRO proteins (see  
XX AAB20108-20) including PRO256. Claimed compositions comprising these  
XX proteins or their agonists are useful for increasing infiltration of T-  
XX inflammatory cells into a tissue of a mammal, stimulating or enhancing an  
XX immune response in a mammal, or increasing the proliferation of T-  
XX lymphocytes in a mammal in response to an antigen. Claimed compositions  
XX comprising the PRO polypeptide or its antagonist have the opposite  
XX effect. A claimed method for treating an immune related disorder, such as  
XX a T cell disorder, involves administering the PRO polypeptide, an agonist  
XX antibody or an antagonist antibody. The disorder is selected from  
XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
XX juvenile chronic arthritis, spondyloarthritis, systemic sclerosis,  
XX idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
XX vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
XX thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
XX disease, demyelinated diseases (such as multiple sclerosis), autoimmune  
XX chronic active hepatitis, primary biliary cirrhosis, granulomatous  
XX hepatitis, sclerosing cholangitis, inflammatory bowel disease (ulcerative

CC colitis and Crohn's disease), gluten-sensitive enteropathy, Whipple's  
CC disease, (auto)immune-mediated skin diseases (such as bullous skin  
CC disease, erythema multiforme and psoriasis), allergic diseases (such as  
CC asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and  
CC urticaria), immunologic diseases of the lung and transplantation  
CC associated diseases (such as graft rejection and graft-versus-host  
CC disease) (all claimed). Claimed methods of diagnosing these disorders  
CC comprise detecting the level of expression of the PRO gene. Also claimed  
CC are a method of identifying a compound capable of inhibiting the  
CC expression or activity of the PRO polypeptide, vectors, host cells,  
CC antibodies and a method of stimulating the proliferation of T-lymphocytes  
CC using PRO256

XX SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 3.94e-114 Length: 2482  
Score: 1163.00 Matches: 205  
Percent Similarity: 99.51% Conservative: 0  
Best Local Similarity: 99.51% Mismatches: 1  
Query Match: 99.66% Indels: 0  
DB: 4 Gaps: 0

US-09-935-390A-23 (1-206) x AAF30055 (1-2482)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
DB 1157 ATGGAAGGGGGCCATCCAGTGTCTCTGGACCTGTTCAGCCACCCAGTTCCTCGAGC 1216  
QY 21 AsnGlyCysCysValLeuSerPheLeuGluCysAspThrProAsnCysProAspAla 40  
DB 1217 AATGGCTGCTGCATCGACAGTTCTCTGGAGTGTGAGACACCCCACTGCCCGGAGCC 1276  
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgHis 60  
DB 1277 TCCAGCAGGCTGCTGTGAAAATACAGAGTGGCTTTCAGCAGGTCCAGCGATCCAT 1336  
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
DB 1337 TTCCCCAGTGCACAAAGGGGCACTCGGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 1396  
QY 81 IleProArgTyrTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100  
DB 1397 ATCCGGGCTGTACTACACCCCTTCAGCGACACTGGCGCGCTTTACCTATGGTGGT 1456  
QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGluGlnCysLeuGluSerCysArgGly 120  
DB 1457 TGTTATGGCAACAGAAACACACTTTGAGGAAGACAGCAGTGGCTCGAGTCTTGTCGGGC 1516  
QY 121 IleSerLysLysAspValPheGlyLeuArgGluLeuPheProIleProSerThrGlySer 140  
DB 1517 ATCTCAAGAGGATGTGTTTGGCTTGGAGCGGGAATCCCATTCAGCAGCAGGCTCT 1576  
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160  
DB 1577 GTGGAGATGGCTGTCAAGTGTTCCTGGTGCATCTGCATTTGTGGTGTAGCCATCTTG 1636  
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisHisHisHis 180  
DB 1637 GGTACTGCTTCTTCAAGAACAGAGAGAGGAGCTTCCACGGACACCCACCCACCCACCA 1696  
QY 181 ProThrProAlaSerThrValSerThrThrThrThrGluAspThrGluHisLeuValTyrAsn 200  
DB 1697 CCCACCCCTGCCAGTCCCACTGTCTCCATACCGAGGACACCGGAGCACCTGGTCTATAAC 1756  
QY 201 HisThrThrArgProLeu 206  
DB 1757 CACACACCCCGGGCCCTC 1774

RESULT 6

AAD16721

ID AAD16721 standard; cDNA; 2482 BP.

XX

AC AAD16721;  
 XX  
 DT 19-NOV-2001 (first entry)  
 XX Human hepatocyte growth factor activator inhibitor, PRO256 cDNA.  
 XX  
 DE Human; PRO256 protein; cardiovascular; endothelial; angiogenic disorder;  
 XX cardiac hypertrophy; trauma; cardiomegaly; age-related macular degeneration;  
 XX gene therapy; angiogenesis; protease activity; hepatocyte growth factor;  
 XX peripheral vascular disease; hepatic; renal injury; nephrotropic; tumor;  
 XX restinosis; tranquilizer; vulnery; cytosstatic; hepatotropic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 PH CDS 188..1177  
 FT /\*tag= a  
 FT /product= "Human hepatocyte growth factor activator  
 FT inhibitor, PRO256"  
 FT sig\_peptide 188..292  
 FT /\*tag= b  
 FT mat\_peptide 293..1174  
 FT /\*tag= c  
 FT /product= "Human mature hepatocyte growth factor  
 FT activator inhibitor, PRO256"  
 FT  
 XX WO200159100-A2.  
 XX  
 XX 16-AUG-2001.  
 XX  
 XX 19-DEC-2000; 2000WO-US034756.  
 XX  
 XX 11-FEB-2000; 2000WO-US003565.  
 XX  
 XX 15-MAR-2000; 2000WO-US006884.  
 XX  
 XX 28-NOV-2000; 2000US-0253665P.  
 XX  
 XX (GENT ) GENENTECH INC.  
 XX  
 XX Gurney AL, Kirchofer DK, Wood WI;  
 XX  
 XX WPI: 2001-541567/60.  
 XX P-PSDB; ARE09332.  
 XX  
 XX An isolated polypeptide designated PRO256 useful for treating a  
 XX cardiovascular, endothelial, or angiogenic disorder.  
 XX  
 XX Claim 40; Fig 1; 124pp; English.  
 XX  
 XX The present invention relates to PRO256 or its agonist/antagonist may be  
 XX used to treat a cardiovascular, endothelial, or angiogenic disorder in a  
 XX mammal, especially a human with cardiac hypertrophy, trauma, a type of  
 XX tumor or age-related macular degeneration. PRO256 may be administered  
 XX together with a cardiovascular, endothelial, or angiogenic agent, a  
 XX chemotherapeutic agent, a growth inhibitory agent, or a cytotoxic agent.  
 XX PRO256 may also be used to treat the disorders above, preferably through  
 XX administration via ex vivo gene therapy. PRO256 or its agonist may be  
 XX used to inhibit endothelial cell growth, angiogenesis or protease  
 XX activity of a hepatocyte growth factor, whereas an antagonist of PRO256  
 XX may be used to stimulate endothelial cell growth, angiogenesis or  
 XX protease activity of a hepatocyte growth factor. Stimulation or  
 XX inhibition of the protease activity of a hepatocyte growth factor is  
 XX preferably carried out where a mammal has a cardiovascular, endothelial,  
 XX or angiogenic disorder selected from peripheral vascular disease, hepatic  
 XX or renal injury or a restinosis disorder. The present sequence is human  
 XX hepatocyte growth factor activator inhibitor, PRO256 cDNA  
 XX  
 XX Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;  
 XX  
 XX Alignment Scores:  
 XX Pred. No.: 3,94e-114 Length: 2482  
 XX Score: 1153.00 Matches: 205  
 XX Percent Similarity: 99.51% Conservative: 0  
 XX Best Local Similarity: 99.51% Mismatches: 1

Query Match: 99.68% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-935-390A-23 (1-206) x AAD16721 (1-2482)  
 QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
 DB 1157 ATGGAAAGCGCCATCCAGTGTCTGACACCTGTGACCCACCCAGTTCGGTGTGACG 1216  
 QY 21 AenGlyCysCysIleAspSerPheLeuGluCysAspSerPheProAsnCysProAspAla 40  
 DB 1217 AATGGCTGCTGCATCGACAGATTCTCTGGAGTGTGACGACACCCCACTGCCCCGAGCC 1276  
 QY 41 SerAspGluAlaAlaCysGluLysPheThrSerGlyPheAspGluLeuGlnArgIleHis 60  
 DB 1277 TCCGACGAGGCTGCTGTGAAAATACACGAGTGTCTTTCAGAGCTTCACGCAATCCAT 1336  
 QY 61 PheProSerAspGlyGlyHisCysValAspLeuProAspThrGlyLeuCysGlySer 80  
 DB 1337 TTCCCCAGTGCACAAAGGCGCACTGCTGGACCTGGCAGACACAGAGCACTCTGCAGAGGAGC 1396  
 QY 81 IleProArgGlyProTyrAsnPropheSerGluHisCysAlaArgPheThrTyrGlyGly 100  
 DB 1397 ATCCCGGCTGTACTACACCCCTTCAGCGACACTGCGCCCTTTACCTATGTGTGT 1456  
 QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120  
 DB 1457 TGTATTGCGCAACAGAAACAACACTTTGAGGAGAGGAGCAGTGCCTCGAGTCTTTGTGCGGC 1516  
 QY 121 IleSerLysValAspValPheGlyLeuArgGluGluPheProSerThrGlySer 140  
 DB 1517 ATCTCCAGAGAGAGTGTGTGGCTTGGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1576  
 QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160  
 DB 1577 GTGGAGATGGCTGTCTCAGTGTCTCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCT 1636  
 QY 161 GlyTyrCysPhePheLysAsnGluArgLysAspPheHisGlyHisHisHisHisHisPro 180  
 DB 1637 GGTACTCTCTCTTTCAGACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1696  
 QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200  
 DB 1697 CCCACCCCTGCGCAGCTCCACCTGTCTCCACTACGAGGAGCAGGAGGAGGAGGAGGAG 1756  
 QY 201 HisThrThrArgProLeu 206  
 DB 1757 CACACACACCCGCCCCCTC 1774  
 RESULT 7  
 ABK40259  
 ID ABK40259 standard; cDNA; 2482 BP.  
 XX  
 AC ABK40259;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE cDNA encoding human PRO256 polypeptide.  
 XX Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;  
 XX leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;  
 XX inflammatory disorder; immune disorder; angiogenic disorder;  
 XX gene therapy; cytosstatic; neuroprotective; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200153486-A1.  
 XX  
 XX 26-JUL-2001.  
 XX  
 XX 11-FEB-2000; 2000WO-US003565.  
 XX  
 XX 08-MAR-1999; 99WO-US005028.

PR 11-MAR-1999; 99US-0123972P.  
 PR 11-MAY-1999; 99US-0133459P.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 22-JUN-1999; 99US-0140450P.  
 PR 22-JUN-1999; 99US-0140453P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 28-JUL-1999; 99US-0146222P.  
 PR 17-AUG-1999; 99US-0149395P.  
 PR 31-AUG-1999; 99US-0151689P.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 05-JAN-2000; 2000WO-US000219.  
 XX (GETH ) GENENTECH INC.  
 XX PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;  
 PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;  
 PI Natanabe CK, Wood WI;  
 XX DR WPI; 2002-205567/26.  
 XX DR P-PSDB; AAU86133.  
 XX PT Thirty five nucleic acids encoding PRO polypeptides, useful for treating  
 PT benign or malignant tumors, leukemias and lymphoid malignancies,  
 PT inflammatory, angiogenic and immunologic disorders.  
 XX PS Claim 50; Fig 11; 302pp; English.  
 XX CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides and the polynucleotide sequences encoding them. The PRO  
 CC polypeptides, agonists, antagonists or anti-PRO antibodies are useful for  
 CC treating benign or malignant tumors (e.g. renal, kidney, bladder, such  
 CC as neuronal, glioma, astrocytoma, lymphoid malignancies, other disorders, such  
 CC as neuroblastoma, glioma, astrocytoma, lymphoid malignancies, other disorders, such  
 CC as stromal and blastocoele disorders, inflammatory, immune and angiogenic  
 CC disorders. The polynucleotide sequences are also useful in gene therapy.  
 CC CC ABK40254-ABK40288 encode for the human PRO polypeptides of the invention  
 XX SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 3.94e-114 Length: 2482  
 Score: 1163.00 Matches: 205  
 Percent Similarity: 99.51% Conservative: 0  
 Best Local Similarity: 99.51% Mismatches: 1  
 Query Match: 99.66% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-935-390A-23 (1-206) x ABK40259 (1-2482)  
 Qy 1 MetGluArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
 Db 1157 ATGGAAAGGCGCCATCCAGTGTGTCTGGACCTGTGAGCCACCCAGTTCGCTCGAGC 1216  
 Qy 21 AsnGlyCysCysIleAspSerPheLeuGluCysAsnAspThrProAsnCysProAsnAla 40  
 Db 1217 AATGGCTGTGCTGATCGAGTTTCTGAGTGTGACGACACCCCACTGCCCGAGCC 1276  
 Qy 41 SerAspGluAlaAlaCysGluLysThrSerGlyPheAspGluLeuGlnArgIleHis 60  
 Db 1277 TCCGACGAGGCTGCTGTGAAAATAACACGAGTGGCTTTGACGAGTTCAGGCGCATCCAT 1336  
 Qy 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
 Db 1337 TTCCCAAGTGCAGAGGCGCTGCTGAGTGTGACCTGCCAGACAGACTCTCGAGGAGAGC 1396  
 Qy 81 IleProArgThrPheAsnProPheSerGluHisCysAlaArgPheThrGlyGly 100  
 Db 1397 ATCCCGCGCTGCTACTACAAACCCCTTCAGGAAACACCTGCGCGCGCTTTACCTATGCTGT 1456

Qy 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120  
 Db 1457 TGTATGGCAACAGAGACACTTTGAGGAAGACAGCAGTGCCTCGAGTCTTGTCGGGC 1516  
 Qy 121 IleSerLysLysAspValPheGlyLeuArgArgGluLeuPheProIleProSerThrGlySer 140  
 Db 1517 ATCTCCAAAGAGGATGTGTTGGCTGAGGCGGGAATCCCATTCACAGCAGAGCTCT 1576  
 Qy 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160  
 Db 1577 GTGGAGATGCTCTCCAGTGTTCCTGGTCTCATCTGCTGCTGCTGCTGCTGCTGCTG 1636  
 Qy 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180  
 Db 1637 GGTACTGCTTCTTCAGAACACAGAGAGGACTTCACGAGACACACACACACACCA 1696  
 Qy 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200  
 Db 1697 CCCACCCCTGCCAGTCCACTGTCTCCACTACGAGGACACAGGACACCTGTGCTATAAC 1756  
 Qy 201 HisThrThrArgProLeu 206  
 Db 1757 CACACACCCGCGCCCTC 1774  
 RESULT 8  
 ABL88092  
 ID ABL88092 standard; cDNA; 2482 BP.  
 XX ABL88092;  
 AC ABL88092;  
 DT 16-MAY-2002 (first entry)  
 XX Human PRO256 cDNA sequence SEQ ID NO:41.  
 XX Human; angiogenesis; cardiant; cytoetic; antiangiogenic; hypotensive;  
 XX gene therapy; antiarteriosclerotic; PRO agonist; PRO antagonist; cancer;  
 XX gene therapy; cardiovascular disorder; endothelial disorder; trauma;  
 XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 XX age-related macular degeneration; arterial restenosis; angina;  
 XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 XX wound healing; chromosome mapping; gene mapping; gene; as.  
 XX Homo sapiens.  
 OS WO200200690-A2.  
 XX 03-JAN-2002.  
 XX 20-JUN-2001; 2001WO-US019692.  
 XX 23-JUN-2000; 2000US-0213637P.  
 XX 20-JUL-2000; 2000US-0219556P.  
 XX 25-JUL-2000; 2000US-0220624P.  
 XX 28-JUL-2000; 2000US-0220664P.  
 XX 02-AUG-2000; 2000US-0222695P.  
 XX 17-AUG-2000; 2000US-0222695P.  
 XX 23-AUG-2000; 2000US-0222695P.  
 XX 24-AUG-2000; 2000US-0222695P.  
 XX 07-SEP-2000; 2000US-0230978P.  
 XX 18-SEP-2000; 2000US-0230978P.  
 XX 18-SEP-2000; 2000US-0230978P.  
 XX 24-OCT-2000; 2000US-0242922P.  
 XX 08-NOV-2000; 2000US-0242922P.  
 XX 10-NOV-2000; 2000US-0242922P.  
 XX 01-DEC-2000; 2000US-0242922P.  
 XX 20-DEC-2000; 2000US-0242922P.  
 XX 22-JAN-2001; 2001US-00767609.  
 XX 28-FEB-2001; 2001US-00796498.

PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006556.  
 PR 09-MAR-2001; 2001US-00802706.  
 PR 14-MAR-2001; 2001US-00808689.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 25-MAY-2001; 2001US-00866028.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 25-MAY-2001; 2001WO-US017092.  
 PR 30-MAY-2001; 2001US-00870574.  
 PR 30-MAY-2001; 2001WO-US017443.  
 PR 01-JUN-2001; 2001WO-US017800.  
 XX (GETH ) GENENTECH INC.  
 XX Baker KP, Ferrara N, Gerber H, Gerritsen MS, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 XX WP; 2002-090516/12.  
 DR P-PSDB; ABB84837.  
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal.  
 XX Claim 2; Fig 41; 565pp; English.  
 XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
 CC antiangiogenic, hypotensive, and antiarteriosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.  
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma), and wound  
 CC healing. The PRO polynucleotides have applications in molecular biology,  
 CC including use as hybridisation probes, and in chromosome and gene  
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the  
 CC exemplification of the present invention  
 XX SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 3.94e-114 Length: 2482  
 Score: 1163.00 Matches: 205  
 Percent Similarity: 99.51% Conservative: 0  
 Best Local Similarity: 99.51% Mismatches: 1  
 Query Match: 99.66% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-935-390A-23 (1-206) x ABL88092 (1-2482)  
 QY 1 MetGluArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
 Db 1157 ATGGAAGGGCCATCCAGTGTGCTCTGGACCTGTGACCCACCCAGTTCGGCTGCAC 1216  
 QY 21 AsnGlyCysGlyLeuSerPheLeuGluCysAspThrProAsnProAspAla 40  
 Db 1217 AATGGCTGTGCAATCAGACAGTTCCTGGAGTGTGACGACACCCCACTGCCCGCAGCC 1276  
 QY 41 SerAspGluAlaCysGluLysThrThrSerGlyPheAspGluLeuGlnArgIleHis 60  
 Db 1277 TCCGACGAGGCTGCTGTGAAATACACAGTGGCTTTGACGAGCTCCAGCGCATTCAT 1336  
 QY 61 PheProSerAspGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
 Db 1337 TTCCCCAGTGACAAAGGGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGC 1396

QY 81 IleProArgTrpTyrTrpAsnPropheSerGluHisCysAlaArgPheThrTyrGlyGly 100  
 Db 1397 ATCCCGCGTGGTACTACAAACCCCTTTCAGCGAACACTGCGCGCTTTTACCTATGTTGGT 1456  
 QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120  
 Db 1457 TGTATGGCAACAGAACCACTTTGAGGAGAGACAGCAGTGCCTCCAGTCTTGTGCGGC 1516  
 QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluLeuPheProIleProSerThrGlySer 140  
 Db 1517 ATCTCCAGAGGAGTGTGTTGGCTTGAAGCGGAAATCCCATTCACAGTCTTGTGCGGC 1576  
 QY 141 ValGluMetAlaValAlaValPheLeuValIleCysValIleValValValAlaIleLeu 160  
 Db 1577 GTGGAGATGGCTGTTCACAGTGTCTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1636  
 QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180  
 Db 1637 GGTACTGTCTTCTTCAAGAACACAGAGAAAGGACTTCCACGGACACCCACCACCCACCA 1696  
 QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200  
 Db 1697 CCCACCCCTGCCAGTCTCCACTGTCTCCACTACGAGACACGAGCAGCTGTGCTTATAAC 1756  
 QY 201 HisThrThrArgProLeu 206  
 Db 1757 CACACCACCGCGCCCTC 1774  
 RESULT 9  
 ID ABL88965 standard; DNA; 2482 BP.  
 AC ABL88965;  
 XX 15-JUL-2002 (first entry)  
 DE cDNA encoding human Pro peptide #5.  
 KW Human; as; gene; PRO; secreted protein; transmembrane protein;  
 KW genetic disorder; tumour; cancer.  
 OS Homo sapiens.  
 XX WO200224888-A2.  
 XX 28-MAR-2002.  
 XX 29-AUG-2001; 2001WO-US027099.  
 PR 01-SEP-2000; 2000US-0229896P.  
 PR 05-SEP-2000; 2000US-0230621P.  
 PR 22-SEP-2000; 2000US-0235147P.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 12-JAN-2001; 2001US-0261878P.  
 PR 16-JAN-2001; 2001US-0261910P.  
 PR 16-JAN-2001; 2001US-0261939P.  
 PR 25-JAN-2001; 2001US-0262150P.  
 PR 02-FEB-2001; 2001US-0264395P.  
 PR 09-FEB-2001; 2001US-0267623P.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 03-MAR-2001; 2001US-0274399P.  
 PR 04-APR-2001; 2001US-0280982P.  
 PR 04-APR-2001; 2001US-0282129P.  
 PR 09-MAY-2001; 2001US-0282199P.  
 PR 25-MAY-2001; 2001US-0290589P.  
 PR 01-JUN-2001; 2001WO-US017092.  
 PR 20-JUN-2001; 2001WO-US017800.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PA (GETH ) GENENTECH INC.



PR 30-MAY-2001; 2001WO-US017443.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 XX (GETH ) GENENTECH INC.  
 PA (BAKE/) BAKER K P.  
 PA (FERR/) FERRARA N.  
 PA (GERE/) GERBER H.  
 PA (GERR/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (MARK/) MARSTERS S A.  
 PA (PANG/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (STEP/) STEPHAN J F.  
 PA (WATA/) WATANABE C K.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 XX WPI: 2002-171999/22.  
 DR P-PSDB; ABL95443.  
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal.  
 XX Claim 1; Fig 41; 567pp; English.  
 XX The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a coding sequence of the invention  
 XX SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 3,948-114 Length: 2482  
 Score: 1163.00 Matches: 205  
 Percent Similarity: 99.51% Conservative: 0  
 Best Local Similarity: 99.51% Mismatches: 1  
 Query Match: 99.66% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-935-390A-23 (1-206) x ABL95581 (1-2482)  
 QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
 Db 1157 ATGGAAGCGCGCATCCAGTGTGCTCTGCGACCTGTGACGCCACCCAGCTTCGGCTGCAGC 1216  
 QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40  
 Db 1217 AATGGCTCTGCTGATGACAGTTCCTGGAGGTGTACGACACCCCACTGCCCGAGGCC 1276  
 QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60  
 Db 1277 TCCGACGAGGCTGCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCAT 1336  
 QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
 Db 1337 TTCCCGAGTGACAAAGCGGCACTGGCTGGACTGCCAGNCACAGGACTCTGCAGGAGGC 1396  
 QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100

Db 1397 ATCCCGCGCTGCTACTACAACCCCTTCAGCGACACTGCGCCGCTTTACCTATGTGTT 1456  
 QY 101 CysTyrGlyAsnLysAsnAspPheGluGluGlnCysLeuGluSerCysArgGly 120  
 Db 1457 TGTATGCAACAGACACACTTTCAGGAGAGGACGAGTCCCTCGAGTCTTGTTCGGGGC 1516  
 QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluLeuProIleProSerThrGlySer 140  
 Db 1517 ATCTCCAAAGAGGATGTTTGGCTGAGGGGGGAAATCCCCATTCACGACACAGGCTCT 1576  
 QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValValValAlaIleLeu 160  
 Db 1577 GGGAGATGGCTGTCACAGTGTTCCTGGTCACTGCTGTTGGTGGTGGTGGTGGTGGT 1636  
 QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisHisHisHis 180  
 Db 1637 GGTACTGCTTCTTCAAGAACCCAGAGAAAGGACTTCCACGAGACACCCACCCACCA 1696  
 QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200  
 Db 1697 CCCACCCCTTCAGCTCCACTGTCTCCACTACCGAGGACACGAGACCTGTCTATAAC 1756  
 QY 201 HistThrArgProLeu 206  
 Db 1757 CACACACCCCGGCCCTC 1774  
 RESULT 11  
 ADA01277  
 ID ADA01277 standard; cDNA; 2482 BP.  
 XX ADA01277;  
 XX 06-NOV-2003 (first entry)  
 XX Human PRO polynucleotide #5.  
 XX Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;  
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;  
 KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;  
 KW microvascular endothelial cell; endothelial cell tube formation;  
 KW sports-related joint problem; articular cartilage defect; osteoarthritis;  
 KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.  
 OS Homo sapiens.  
 XX US2003068779-A1.  
 XX 10-APR-2003.  
 XX 16-SEP-2002; 2002US-00245107.  
 XX 09-MAY-2001; 2001US-0290589P.  
 XX 29-AUG-2001; 2001WO-US027099.  
 XX 18-JUL-2002; 2002US-00197942.  
 XX (GETH ) GENENTECH INC.  
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
 PI Fong S;  
 XX WPI: 2003-625484/59.  
 XX P-PSDB; ADA01278.  
 XX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for  
 PT stimulating proliferation of human microvascular endothelial cells, and  
 PT PRO5018 polypeptide useful for stimulating proliferation of chondrocyte  
 PT cells.  
 XX Claim 2; Fig 9; 307pp; English.  
 XX The invention relates to isolated human PRO polypeptides (secreted and  
 CC transmembrane polypeptides) and the polynucleotides encoding them. The

invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumor necrosis factor- $\alpha$  (TNF- $\alpha$ ) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for inducing endothelial cell tube formation and for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence represents a human PRO polynucleotide of the invention.

SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 3.94e-114 Length: 2482  
Score: 1163.00 Matches: 205  
Percent Similarity: 99.51% Conservative: 0  
Best Local Similarity: 99.51% Mismatches: 1  
Query Match: 99.66% Indels: 0  
DB: 8 Gaps: 0

US-09-935-390A-23 (1-206) x ADA01277 (1-2482)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
Db 1157 ATGGAAGGCGCCATCAGTGTCTTGGRCCTGTGAGCCACCCAGTTCGGTCCGAC 1216  
QY 21 AsnGlyCysCysLeuSerPheLeuGluCysAspThrProAsnCysProAspAla 40  
Db 1217 AATGGCTGTGTCATCGACATTTCTGTGAGTGTGACGACACCCCACTGCCGAGCGC 1276  
QY 41 SerAspGluAlaAlaCysGluValSerThrSerGlyPheAspGluLeuGlnArgIleHis 60  
Db 1277 TCGACAGCGTCCCTGTGAAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1336  
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
Db 1337 TTCCCGAGTGACAAAGGCGCACTGGTGACCTGCCAGACACAGACTCTCCAGAGAGCC 1396  
QY 81 IleProArgTrpTyrTrpAsnProPheSerGluHisCysAlaArgPheThrTrpGlyGly 100  
Db 1397 ATCCCGCGTGGTACTACACCCCTTCACGCAACACTGCGCCCGCTTTACCTATGCTGT 1456  
QY 101 CysTrpGlyValNlyAsnAsnPheGluGluGluGlnCysLeuGluSerCysArgGly 120  
Db 1457 TGTATGCAACAGACACAACTTTAGGAGAGAGCGAGTGGCTCGAGTCTTGTGCGGCG 1516  
QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140  
Db 1517 ATCTCCAGAGAGTGTGTGGCTTGAGCGGGAAATCCCATTTCCAGACACAGGCTCT 1576  
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160  
Db 1577 GTGGAGATGGCTGTACAGTGTCTCTGTCATCTGATGTTGGTGGTATGCCATCTTG 1636  
QY 161 GlyTrpCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisPro 180  
Db 1637 GGTACTGCTCTTCAAGAACCCAGAGAAAGGACTTCCAGCGACACACACCCACCA 1696  
QY 181 ProThrProLysSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200  
Db 1697 CCCACCCCTGCGAGTCTCCACTGCTCCACTCCGAGGACCGAGGACCTGGTCTATAAC 1756  
QY 201 HisThrThrArgProLeu 206

Db 1757 CACACACCGCGCCCTC 1774  
RESULT 12  
ADA43706  
ID ADA43706 standard; cDNA; 2482 BP.  
AC ADA43706;  
XX  
DT 20-NOV-2003 (first entry)  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.  
KW ss; gene; human; PRO; secreted protein; transmembrane protein;  
KW endothelial cell tube formation; chondrocyte cell differentiation;  
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;  
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;  
KW liver tumour; cytostatic; vaccine.  
XX  
OS Homo sapiens.  
XX  
PN US2003064474-A1.  
XX  
PD 03-APR-2003.  
XX  
PF 16-SEP-2002; 2002US-00245859.  
XX  
PR 29-AUG-2001; 2001WO-US027099.  
PR 18-JUL-2002; 2002US-00197942.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
PI Pong S;  
XX  
DR WPI: 2003-605867/57.  
DR P-PSDB; ADA43707.  
XX  
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or  
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in  
PT generating antisense RNA and DNA, and in gene therapy.  
XX  
PS Claim 2; Fig 9; 308pp; English.

CC The invention relates to an isolated secreted/transmembrane (PRO)  
CC polypeptide, having at least 80% sequence identity to a sequence selected  
CC from any one of the 57 amino acid sequences given in specification, or to  
CC a sequence encoded by a nucleic acid molecule selected from any one of  
CC the nucleic acids deposited under any of the ATCC accession numbers given  
CC in specification, or a sequence having at least 80% identity to PRO  
CC lacking its associated signal peptide, an extracellular domain of PRO  
CC with or without its associated signal peptide. Also included are vectors,  
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding  
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by  
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,  
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and  
CC an oligonucleotide probe derived from any one of the above nucleotide  
CC sequences. PRO6018 polypeptide is useful for stimulating the  
CC proliferation or differentiation of chondrocyte cells. PRO313, PRO20080  
CC and PRO21383 polypeptides are useful for stimulating the proliferation of  
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006  
CC polypeptides are useful for inhibiting the proliferation of human  
CC microvascular endothelial cells. PRO polypeptides are useful for  
CC detecting the presence of tumour in a mammal, including tumours of lung,  
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,  
CC PRO189, PRO4499, PRO6308, PRO10275, PRO21207, PRO20933 and  
CC PRO34274 polypeptides are useful for inducing endothelial cell tube  
CC formation. PRO or the antibody are useful in the preparation of a  
CC medicament for treating a condition responsive to PRO polypeptide. The  
CC oligonucleotide probes are useful for isolating genomic and cDNA  
CC nucleotide sequences, for measuring or detecting the expression of an  
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a

CC hybridisation probe, in chromosome and gene mapping, in the generation of  
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and  
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The  
CC present sequence encodes a PRO protein.

XX SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 3,94e-114 Length: 2482  
Score: 1163.00 Matches: 205  
Percent Similarity: 99.51% Conservatives: 0  
Best Local Similarity: 99.51% Mismatches: 1  
Query Match: 99.66% Indels: 0  
DB: 8 Gaps: 0

US-09-935-390A-23 (1-206) x ADA43706 (1-2482)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
Db 1157 ATGGAAGCGCGCATCCAGTGTCTGCGCACCTGTGAGCCACCCAGTTCGGCTGCAGC 1216  
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40  
Db 1217 AATGCTGCTCATCGACAGTTTCTGGAGTGTGACGACACCCCAACTGCCCCGACGCC 1276  
QY 41 SerAspGluAlaAlaCysGluLeuValThrSerGlyPheAspGluLeuGlnArgIleHis 60  
Db 1277 TCCGACGAGGCTGCTGTGAAATAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1336  
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
Db 1337 TTCCCAAGTGCACAAAGGCGACTGGTGGACCTGCCACACACAGGACTCTCCAAAGGAGC 1396  
QY 81 IleProArgThrPheValAsnProPheSerGluHisCysAlaArgPheThrThrGlyGly 100  
Db 1397 ATCCCGGCGTGGTACTACACCCCTTCAGGACACACTGCGCCGCTTACTATGTGGT 1456  
QY 101 CysThrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120  
Db 1457 TGTTATGCAACAAAGAACAACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGC 1516  
QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluLeuProIleProSerThrGlySer 140  
Db 1517 ATCTCAAGAGGATGTTGTTGGCTGAGCGGGAAATCCCATTCACACACAGGCTCT 1576  
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysLeuValValValAlaIleLeu 160  
Db 1577 GTGAGATGCTGTCACAGTGTCTCTGCTCATCTGCTATTCGTTGCTGTAGCATCTTG 1636  
QY 161 GlyThrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisProPro 180  
Db 1637 GGTTACTGCTTCTCAAGAACCCAGAGGAGGAGACTTCCACGACACACACCCACCA 1696  
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200  
Db 1697 CCCACCCCTCCAGCTCCACTGTCTCCACTACCGAGGACGACGAGCAGCTGTGTATAC 1756  
QY 201 HisThrThrArgProLeu 206  
Db 1757 CACACACCCCGCCCCCTC 1774

## RESULT 13

ADA43474

ID ADA43474 standard; cDNA; 2482 BP.

XX ADA43474;

AC 20-NOV-2003 (first entry)

DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.

XX ss; gene; human; PRO; secreted protein; transmembrane protein;  
KW endothelial cell tube formation; chondrocyte cell differentiation;

KW

KW

KW

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PA

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microvascular endothelial cell; tumour; lung tumour; colon tumour;  
breast tumour; prostate tumour; rectal tumour; kidney tumour;  
liver tumour; cytostatic; vaccine.

Homo sapiens.

US2003073196-A1.

17-APR-2003.

18-SEP-2002; 2002US-00246210.

04-APR-2001; 2001US-0282199P.

29-AUG-2001; 2001WO-US027099.

18-JUL-2002; 2002US-0017942.

(GETH ) GENENTECH INC.

Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;

Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI, Zhang Z;

Pong S;

WPI: 2003-743814/70.

P-PSDB; ADA43475.

New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or

PRO21383 useful for stimulating the proliferation or differentiation of

chondrocyte cells and detecting the presence of a tumor in a mammal.

Claim 2; Fig 9; 307pp; English.

The invention relates to an isolated secreted/transmembrane (PRO)

polypeptide, having at least 80% sequence identity to a sequence selected

from any one of the 57 amino acid sequences given in specification, or to

a sequence encoded by a nucleic acid molecule selected from any one of

the nucleic acids deposited under any of the ATCC accession numbers given

in specification, or a sequence having at least 80% identity to PRO

lacking its associated signal peptide, an extracellular domain of PRO

with or without its associated signal peptide. Also included are vectors,

transformed host cells, anti-PRO antibodies, the nucleic acids encoding

PRO, PRO fusion proteins, inducing endothelial cell tube formation (by

administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,

PRO10275, PRO1207, PRO20933 or PRO34274 polypeptide or its agonist) and

an oligonucleotide probe derived from any one of the above nucleotide

sequences. PRO6018 polypeptide is useful for stimulating the

proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080

and PRO21393 polypeptides are useful for stimulating the proliferation of

human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006

polypeptides are useful for inhibiting the proliferation of human

microvascular endothelial cells. PRO polypeptides are useful for

detecting the presence of tumor in a mammal, including tumours of lung,

colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,

PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and

PRO34274 polypeptides are useful for inducing endothelial cell tube

formation. PRO or the antibody are useful in the preparation of a

medicament for treating a condition responsive to PRO polypeptide. The

oligonucleotide probes are useful for isolating genomic and cDNA

nucleotide sequences, for measuring or detecting the expression of an

associated gene, and as antisense probes. PRO nucleic acid is useful as a

hybridisation probe, in chromosome and gene mapping, in the generation of

antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and

PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The

present sequence encodes a PRO protein.

Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 3,94e-114 Length: 2482  
Score: 1163.00 Matches: 205  
Percent Similarity: 99.51% Conservatives: 0  
Best Local Similarity: 99.51% Mismatches: 1  
Query Match: 99.66% Indels: 0  
DB: 8 Gaps: 0



US-09-935-390A-23 (1-206) x ADA43474 (1-2482)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
 Db 1157 ATGGAAAGGCGCCATCCAGTGTCTCTGGCACTGTTCAGCCACCCAGCCAGTTCCTCGCTGACG 1216  
 QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40  
 Db 1217 AATGGCTGTCTGTCATCGACAGTTCCTGGAGTGTGACGACACCCCGCACTGCCCCGACGCG 1276  
 QY 41 SerAspGluAlaAlaCysGluLysTyThrSerGlyPheAspGluLeuGlnArgIleHis 60  
 Db 1277 TCCGACGAGGTGCTCTGTGAAATAACAGAGTGGCTTTCAGCAGTTCGAGCCGATCCAT 1336  
 QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
 Db 1337 TTCCCGAGTGCACAAAGGCGCACTGGCTGGACCTGCCAGACACAGGACTCTGCCAAGGAGAGC 1396  
 QY 81 IleProArgTrpTyThrAsnProPheSerGluHisCysAlaArgPheThrTyrdGlyGly 100  
 Db 1397 ATCCGCGCTGTACTACACCCCTTCAGCGACACTGGCCGCGCTTACCTATGTGTGT 1456  
 QY 101 CysTyrglyAsnLysAsnAsnGluGluGlnCysLeuGlnCysLeuGluSerCysArgGly 120  
 Db 1457 TGTATATGCGCAACAAAGAACTTTGAGGAAAGAGCAGGAGTCCCTCGAGTCTTGTCCGCGC 1516  
 QY 121 IleSerLysLysAspValPheGlyLeuArgGluLeuProIleProSerThrGlySer 140  
 Db 1517 ATCTCCAGAGAGTGTGTGGCTGAGCGGGAATCCCATTCAGGACAGGCTCT 1576  
 QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeu 160  
 Db 1577 GTGGAGATGGCTGTTCACAGTGTCTCTGTCATCTGCTGTTGTGTGTGTGTGTGTGTGTGT 1636  
 QY 161 GlyTyrcysPhePheLysAsnGlnAtqLysAspPheHisGlyHisIleHisIleProPro 180  
 Db 1637 GSTTACTGTTCTTCAAGAACCCAGAGAGAGACTTCCAGGACACACACACACACACAC 1696  
 QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyra 200  
 Db 1697 CCCACCCCTCCGAGTCTCACTGTCTCCACTACCGGAGACACGAGCAGCTGTGTCTATAC 1756  
 QY 201 HisThrThrArgProLeu 206  
 Db 1757 CACACACACCGGCCCCCTC 1774

## RESULT 14

ADA01149  
 ID ADA01149 standard; cDNA; 2482 BP.

XX AC ADA01149;  
 XX DT 06-NOV-2003 (first entry)  
 XX DX Human PRO polynucleotide #5.  
 XX DE Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;  
 XX KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;  
 XX KW cancer; lung; colon; breast; prostate; rectum; kidney; liver;  
 XX KW microvascular endothelial cell; endothelial cell tube formation.  
 XX OS Homo sapiens.  
 XX FN US2003068782-A1.  
 XX PD 10-APR-2003.  
 XX PF 16-SEP-2002; 2002US-00245851.  
 XX PR 27-APR-1999; 99US-0131271P.  
 XX PR 29-OCT-1999; 99US-0162506P.  
 XX PR 02-DEC-1999; 99WO-US028551.

29-AUG-2001; 2001WO-US027099.  
 18-JUL-2002; 2002US-00197942.

(GETH) GENENTECH INC.

Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC,  
 Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
 For S;  
 WPI; 2003-625487/59.  
 P-PSDB; ADA01150.

Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the  
 preparation of a medicament for treating a condition responsive to PRO  
 polypeptide, and as therapeutic agents e.g. vaccines.

Claim 2; Fig 9; 308pp; English.

The invention relates to isolated human PRO polypeptides (secreted and  
 transmembrane polypeptides) and the polynucleotides encoding them. The  
 invention also relates to an antibody which specifically binds to a PRO  
 polypeptide, a method for stimulating the release of tumour necrosis  
 factor-alpha (TNF-alpha) from human blood, a method for stimulating the  
 proliferation or differentiation of chondrocyte cells and a method for  
 detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,  
 prostate, rectal, kidney and liver tumours). The polynucleotides are  
 useful in molecular biology, including uses as hybridisation probes, in  
 chromosome and gene mapping, in generating antisense RNA and DNA and in  
 gene therapy. The polynucleotides may also be used in preparing PRO  
 polypeptides by recombinant techniques and in generating either  
 transgenic animals or knock-out animals which are useful in the  
 development and screening of therapeutically useful reagents. The PRO  
 polypeptides or antibodies are used in preparing a medicament for  
 treating a condition responsive to the polypeptides or antibodies, such  
 as tumours, for stimulating and inhibiting proliferation of human  
 microvascular endothelial cells and for inducing endothelial cell tube  
 formation. This sequence represents a human PRO polynucleotide of the  
 invention.

Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 3.94e-114 Length: 2482  
 Score: 1163.00 Matches: 205  
 Percent Similarity: 99.51% Conservative: 0  
 Best Local Similarity: 99.51% Mismatches: 1  
 Query Match: 99.66% Indels: 0  
 DB: Gaps: 0

US-09-935-390A-23 (1-206) x ADA01149 (1-2482)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
 Db 1157 ATGGAAAGGCGCCATCCAGTGTCTCTGGCACTGTTCAGCCACCCAGCCAGTTCCTCGCTGACG 1216  
 QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40  
 Db 1217 AATGGCTGTCTGTCATCGACAGTTCCTGGAGTGTGACGACACCCCGCACTGCCCCGACGCG 1276  
 QY 41 SerAspGluAlaAlaCysGluLysTyThrSerGlyPheAspGluLeuGlnArgIleHis 60  
 Db 1277 TCCGACGAGGTGCTCTGTGAAATAACAGAGTGGCTTTCAGCAGTTCGAGCCGATCCAT 1336  
 QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
 Db 1337 TTCCCGAGTGCACAAAGGCGCACTGGCTGGACCTGCCAGACACAGGACTCTGCCAAGGAGAGC 1396  
 QY 81 IleProArgTrpTyThrAsnProPheSerGluHisCysAlaArgPheThrTyrdGlyGly 100  
 Db 1397 ATCCGCGCTGTACTACACCCCTTCAGCGACACTGGCCGCGCTTACCTATGTGTGT 1456  
 QY 101 CysTyrglyAsnLysAsnAsnGluGluGlnCysLeuGlnCysLeuGluSerCysArgGly 120

Db 1457 TGTATGGCAACAGAACACCTTTCAGGAGCAGCAGTCCCTGAGTCTTGTCGGCGC 1516  
 QY 121 IleSerLysLysAspValPheGlyLeuHrgArgGluLeuProIleProSerThrGlySer 140  
 Db 1517 ATCTCAAGAGGATGTGTTGGCTGAGCGGGAATCCCATCCAGACAGGCTCT 1576  
 QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeu 160  
 Db 1577 GTGGAGATGGCTGTACAGATGTCTCTGTCATCTGTCATGTGGTGGTGGATCCATCTTG 1636  
 QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180  
 Db 1637 GGTACTGCTCTTCTCAAGAACAGAGAAAGGACTTCCACGACACCCACCCACCA 1696  
 QY 181 ThrThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200  
 Db 1697 CCACCCCTCCAGCTCCACGTCTCCTGCTCCCTACCGAGGACACGGAGCAGCTGGTCTATAAC 1756  
 QY 201 HisThrThrArgProLeu 206  
 Db 1757 CACACACCCGCGCCCTC 1774

## RESULT 15

ADA01033

ID ADA01033 standard; cDNA; 2482 BP.

XX

AC ADA01033;

XX 06-NOV-2003 (first entry)

XX Human cDNA encoding secreted/transmembrane polypeptide PRO256.

XX ss; gene; human; PRO; secreted protein; transmembrane polypeptide PRO256.

XX endothelial cell tube formation; chondrocyte cell differentiation;

XX microvascular endothelial cell; tumour; lung tumour; colon tumour;

XX breast tumour; prostate tumour; rectal tumour; kidney tumour;

XX liver tumour; cytostatic; vaccine.

XX Homo sapiens.

XX US2003068780-A1.

XX 10-APR-2003.

XX 16-SEP-2002; 2002US-00245143.

XX 02-AUG-2000; 2000US-0222695P.

XX 20-JUN-2001; 2001WO-US019632.

XX 29-AUG-2001; 2001WO-US027099.

XX 18-JUL-2002; 2002US-00197942.

XX (GETH) GENENTECH INC.

XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;

XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WL, Zhang Z;

XX Fong S;

XX WPI; 2003-625485/59.

XX P-PSDB; ADA01034.

XX Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the

XX preparation of a medicament for treating a condition responsive to PRO

XX polypeptide, and as therapeutic agents e.g. vaccines.

XX Claim 2; Fig 9; 307pp; English.

XX The invention relates to an isolated secreted/transmembrane (PRO)

XX polypeptide, having at least 80% sequence identity to a sequence selected

XX from any one of the 57 amino acid sequences given in specification, or to

XX a sequence encoded by a nucleic acid molecule selected from any one of

XX the nucleic acids deposited under any of the ATCC accession numbers given

XX in specification, or a sequence having at least 80% identity to PRO

XX lacking its associated signal peptide, an extracellular domain of PRO

CC with or without its associated signal peptide. Also included are vectors,  
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding  
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by  
 CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,  
 CC PRO10275, PRO1207, PRO20933 or PRO34274 polypeptide or its agonist) and  
 CC an oligonucleotide probe derived from any one of the above nucleotide  
 CC sequences. PRO6018 polypeptide is useful for stimulating the  
 CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080  
 CC and PRO1393 polypeptides are useful for stimulating the proliferation of  
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006  
 CC polypeptides are useful for inhibiting the proliferation of human  
 CC microvascular endothelial cells. PRO polypeptides are useful for  
 CC detecting the presence of tumour in a mammal, including tumours of lung,  
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,  
 CC PRO189, PRO4499, PRO308, PRO6000, PRO10275, PRO1207, PRO20933 and  
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube  
 CC formation. PRO or the antibody are useful in the preparation of a  
 CC medicament for treating a condition responsive to PRO polypeptide. The  
 CC oligonucleotide probes are useful for isolating genomic and cDNA  
 CC nucleotide sequences, for measuring or detecting the expression of an  
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a  
 CC hybridisation probe, in chromosome and gene mapping, in the generation of  
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and  
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The  
 CC present sequence encodes a PRO protein.

XX

SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 3,948-114 Length: 2482  
 Score: 1163.00 Matches: 205  
 Percent Similarity: 99.51% Conservatives: 0  
 Best Local Similarity: 99.51% Mismatches: 1  
 Query Match: 99.66% Indels: 0  
 DB: 8 Gaps: 0

US-09-935-390A-23 (1-206) x ADA01033 (1-2482)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
 Db 1157 ATGGAAAGCGCCATCCAGTGTCTTGGCACCTGTTCAGCCACCCAGTTCCTCGTCGAGC 1216  
 QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40  
 Db 1217 AATGCTGCTGCATCGACAGTTTCTTGGAGTGTGACGACACCCCACTGCCCCGACGCC 1276  
 QY 41 SerAspGluAlaAlaCysGluLysThrThrSerGlyPheAspGluLeuGlnArgIleHis 60  
 Db 1277 TCCGACGAGGCTGCTGTGAATAATACACGAGTGTGCTTTCAGAGCTCCAGCGCATCCAT 1336  
 QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
 Db 1337 TTCCTCCAGTGCACAAAGGCGCACTGGTGGACCTGCGACACACAGAGACTCTGCAAGGAGC 1396  
 QY 81 IleProArgThrTyrTyrAsnProPheSerGluHisCysAlaArgPheThrThrGlyGly 100  
 Db 1397 ATCCCGCGCTGTGTACTACACCCCTTCAGCGAACACTGCGCCCGCTTACCTATGTTGGT 1456  
 QY 101 CysTyrGlyAsnLysAsnAspPheGluGluGlnGlnCysLeuGluSerCysArgGly 120  
 Db 1457 TGTATGCAACACAGACACACTTTGGAGAGAGACAGCAGTGCCTCGAGTCTTGTTCGCGC 1516  
 QY 121 IleSerLysLysAspValPheGlyLeuArgGluLeuProIleProSerThrGlySer 140  
 Db 1517 ATCTCAAGAGGATGTGTTGGCTTGGCGGGAATCCCATTCACGACACAGGCTCT 1576  
 QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeu 160  
 Db 1577 GTGGAGATGGCTGTACAGTGTCTCTGTCATCTGTCATTTGGTGGTGGTAGCATCTTG 1636  
 QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180  
 Db 1637 GGTACTGCTCTTCTCAAGAACAGAGAAAGGACTTCCACGACACCCACCCACCA 1696

Qy	181	ProThrProAlaSerSerThrValSerThrThrCluAspThrCluHisLeuValTyrAsn	200
Db	1697	CCCCCCCCCTGCCAGCTCCACTGCTCCACTACCGAGACACGGAGCACCCTGGTCTATAAC	1756
Qy	201	HisThrThrArgProLeu	206
Db	1757	CACACCACCCGGCCCTC	1774

Search completed: April 22, 2004, 08:29:56  
 Job time : 401 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 22, 2004, 07:00:24 ; Search time 3729 Seconds  
(without alignments)  
2394.386 Million cell updates/sec

Title: US-09-935-390A-23

Perfect score: 1167

Sequence: 1 MERRHPVCSGTQCTQPCRS.....TVSTEDTEHLVYNHTREL 206

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgm2\_1/USPTO\_spool/US09935390/runat\_20042004\_144849\_10383/app\_query.fasta\_1.391  
-DB=GenEmbl -QMT=blastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pt -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6  
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Database :

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41: em\_htgo\_other:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1167	100.0	1505	6	BD063229 Secreted
2	1167	100.0	1542	6	AR148260 Sequence
3	1167	100.0	1542	6	E12898 Human cDNA
4	1167	100.0	1542	6	E21838 Preventive
5	1167	100.0	1542	6	AR237449 Sequence
6	1167	100.0	1542	9	BT007425 Homo sapi
7	1167	100.0	1542	12	BT009882 Synthetic
8	1167	100.0	1870	6	AR123705 Sequence
9	1167	100.0	1870	6	BD205506 Human pro
10	1167	100.0	2297	9	BC004140 Homo sapi
11	1167	100.0	2399	9	AB000095 Homo sapi
12	1167	100.0	2486	9	BC018702 Homo sapi
13	1163	99.7	2370	9	AY296715 Homo sapi
14	1163	99.7	2482	6	AX077023 Sequence
15	1163	99.7	2482	6	AX201332 Sequence
16	1163	99.7	2482	6	AX211596 Sequence
17	1163	99.7	2482	6	AX454456 Sequence
18	1163	99.7	2482	6	AX490934 Sequence
19	1163	99.7	2482	6	AX574482 Sequence
20	1163	99.7	2482	9	AY358969 Homo sapi
21	999	85.6	2173	10	BC005769 Mus muscu
22	999	85.6	2534	10	BC053341 Mus muscu
23	989	84.7	2228	10	AF099018 Mus muscu
24	692.5	59.3	115793	9	AC025166 Homo sapi
25	692.5	59.3	178248	9	AC012476 Homo sapi
26	647	55.4	816	6	BD241927 Compounds
27	647	55.4	816	6	AR237110 Sequence
28	647	55.4	816	6	AR260603 Sequence
29	647	55.4	816	6	AR278134 Sequence
30	647	55.4	816	6	AR366830 Sequence
31	647	55.4	816	6	AR370726 Sequence
32	647	55.4	816	6	AR392231 Sequence
33	647	55.4	816	6	AR399866 Sequence
34	647	55.4	816	6	AR405133 Sequence
35	647	55.4	816	6	AX106233 Sequence
36	647	55.4	816	6	AX140524 Sequence
37	647	55.4	816	6	AX200384 Sequence
38	647	55.4	816	6	AX267040 Sequence
39	647	55.4	816	6	BD070163 Compounds
40	584	50.0	1037	6	AX067320 Sequence
41	572	49.0	760	6	BD241950 Compounds
42	572	49.0	760	6	AR217133 Sequence
43	572	49.0	760	6	AR250626 Sequence
44	572	49.0	760	6	AR278157 Sequence
45	572	49.0	760	6	AR366853 Sequence

# ALIGNMENTS

RESULT 1

BD063229  
LOCUS BD063229  
DEFINITION Secreted human proteins.  
ACCESSION BD063229  
VERSION BD063229.1 GI:22608832  
KEYWORDS JP 2001505783-A/4.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 1505)  
AUTHORS Escobedo, J., Hu, Q., Garcia, P., Williams, L.T. and Kothakota, S.  
TITLE Secreted human proteins  
JOURNAL Patent: JP 2001505783-A 4 08-MAY-2001;  
COMMENT CHIRON CORP  
PN JP 2801505783-A/4  
PD 08-MAY-2001  
PF 11-DEC-1997 JP 1998526977  
PR 11-DEC-1996 US 60/032757  
PI JAIME ESCOBEDO, QUIANJIN HU, PABLO GARCIA, LEWIS T WILLIAMS PI  
PC C12N15/12, C12N15/62, C12N15/85, C12N5/10, C12N1/21, C07K14/47, PC  
C07K16/18  
CC Strandedness: Single;  
FH Key Location/Qualifiers.  
CC Topology: Linear;  
FH Key Location/Qualifiers  
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/organism="unidentified"  
/mol\_type="genomic DNA"  
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source  
ORIGIN  
Alignment Scores:  
Pred. No.: 4.59e-117 Length: 1505  
Score: 1167.00 Matches: 206  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-09-935-390A-23 (1-206) x BD063229 (1-1505)  
QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
DB 171 ATGGAAGGGCGCATCCAGTGTCTCGGCACCTGTCTGACCCACCCAGTTCGCTGCGC 230  
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40  
DB 231 AATGGCTGCTGCATCGACAGTTCCTGGAGTGTGACGACACCCGCCACTGCCCCGAGCC 290  
QY 41 SerAspGluAlaAlaCysGluLysThrSerGlyPheAspGluLeuGlnArgIleHis 60  
DB 291 TCCGACGAGCTGCTGTGAAAATAACAGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 350  
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
DB 351 TTCCGACGACGAAAGGGCACTCGTGGACCTCCAGACACAGACTCTGCAAGGAGAGC 410  
QY 81 IleProArgTrpTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100  
DB 411 ATCCCGCGCTGGTACTACACCCCTTCAGCAACACTGCGCCGCTTTACCTATGGTGT 470  
QY 101 CysTyrGlyAsnLysAsnAsnAsnGluGluGluGlnCysLeuGluSerCysArgGly 120  
DB 471 TGTATGGCAACAGAAACAACTTTGAGGAGAGCAGCAGTGGCTCGAGTCTTGTGCGGC 530  
QY 121 IleSerLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140  
DB 531 ATCTCCAGAGAGTGTGTGGCTGAGCGGAAATCCCATTCCTCCAGCACAGGCTCT 590  
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeu 160  
DB 591 GTGAGATGGCTGCTCGCAGTGTCTCGGTCATCTGCATTTGTGGTGTGTGATCCATCTTG 650

QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180  
DB 551 GGTTACTGCTTCTTCAAGAACACAGAAAGAGACTTCCAGGACACCCACCCACCA 710  
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200  
DB 711 CCACCCCTGCGAGTCCACTGCTCTCCACTACCGAGACACGAGACACCTGGTCTATAAC 770  
QY 201 HisThrThrArgProLeu 206  
DB 771 CACACCACGCGGCCCTC 788  
RESULT 2  
ARI48260  
LOCUS ARI48260 1542 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 8 from patent US 6225081.  
ACCESSION ARI48260  
VERSION ARI48260.1 GI:15112350  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1542)  
AUTHORS Shimomura, I., Kawaguchi, T., Kitamura, N. and Miyazawa, K.  
TITLE Protein, DNA coding for same and method of producing the protein  
JOURNAL Patent: US 6225081-A 8 01-MAY-2001;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"  
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Alignment Scores:  
Pred. No.: 4.72e-117 Length: 1542  
Score: 1167.00 Matches: 206  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
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DB 922 ATGGAAGGGCGCATCCAGTGTCTCGGCACCTGTGACCCACCCAGTTCGCTGCGC 981  
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40  
DB 982 AATGGCTGCTGCATCGACAGTTCCTGGAGTGTGACGACACCCGCCACTGCCCCGAGCC 1041  
QY 41 SerAspGluAlaAlaCysGluLysThrSerGlyPheAspGluLeuGlnArgIleHis 60  
DB 1042 TCCGACGAGCTGCTGTGAAAATAACAGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1101  
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
DB 1102 TTCCGACGACGAAAGGGCACTCGTGGACCTCCAGACACAGACTCTGCAAGGAGAGC 1161  
QY 81 IleProArgTrpTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100  
DB 1162 ATCCCGCGCTGGTACTACACCCCTTCAGCAACACTGCGCCGCTTTACCTATGGTGT 1221  
QY 101 CysTyrGlyAsnLysAsnAsnAsnGluGluGluGlnCysLeuGluSerCysArgGly 120  
DB 1222 TGTATGGCAACAGAAACAACTTTGAGGAGAGCAGCAGTGGCTCGAGTCTTGTGCGGC 1281  
QY 121 IleSerLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140  
DB 1282 ATCTCCAGAGAGTGTGTGGCTGAGCGGAAATCCCATTCCTCCAGCACAGGCTCT 1341  
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeu 160



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 FT mat peptide 106..1542.  
 FEATURES Location/Qualifiers  
 source 1..1542  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4.72e-117 Length: 1542  
 Score: 1167.00 Matches: 206  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-935-390A-23 (1-206) x E21838 (1-1542)

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 DB 982 AATGGCTGCTGCATCGACATTTCTGGAGTGTGACGACACCCCACTGCCCGACGCC 1041  
 QY 41 SerAspGluAlaCysGluIleAspThrSerGlyPheAspGluLeuGlnArgIleHis 60  
 DB 1042 TCCGACGAGCTGCTGTGAAAATAACAGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1101  
 QY 61 PheProSerAspGlyHisCysValAspLeuProAspThrGlyLeuCysGlySer 80  
 DB 1102 TTCCCGAGTGCAGAGGCGACTCGGTGGACCTCCAGACACAGACTCTGCAAGGAGAGC 1161  
 QY 81 IleProArgTrpTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100  
 DB 1162 ATCCCGCTGTGTACTACACCCCTTCAGGACACTGCGCGCTTTTACCTATGTGT 1221  
 QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnCysLeuGluSerCysArgGly 120  
 DB 1222 TGTATGGCAACAGAACAACTTTGAGAGAGACAGACAGTGCCTCGAGTCTGTGCGGC 1281  
 QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140  
 DB 1282 ATCTCCAGAGGATGTGTTGSCCTGAGCGGGAATCCCATTTCCAGCACAGGCTCT 1341  
 QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160  
 DB 1342 GTGGAGATGCTGTGCAAGTGTCTGTCATCTGCAATGTGTGTGTGTAGCATCTTG 1401  
 QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180  
 DB 1402 GGTACTGCTTCTTCAGAACCCAGAGAGGACTTCCAGGACACCCACCCACCA 1461  
 QY 181 ProThrProAlaSerSerThrValSerThrGluAspThrGluHisLeuValTyrAsn 200  
 DB 1462 CCCACCCCTGCCAGTCTGCTCCACTACCGAGGACAGGACGACCTGCTGTATAC 1521  
 QY 201 HisThrThrArgProLeu 206  
 DB 1522 CACACCCCGGCCCTC 1539

## RESULT 5

AR237449  
 LOCUS AR237449 1542 bp mRNA linear PAT 20-DEC-2002  
 DEFINITION Sequence 8 from patent US 6465622.  
 ACCESSION AR237449  
 VERSION AR237449.1 GI:27282185  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.

## REFERENCE

1 (bases 1 to 1542)  
 Shimomura,T., Kawaguchi,T., Kitamura,N. and Miyazawa,K.  
 TITLE Protein, DNA coding for same and method of producing the protein  
 JOURNAL Patent: US 6465622-A 8 15-OCT-2002;  
 FEATURES Location/Qualifiers  
 source 1..1542  
 /organism="unknown"  
 /mol\_type="mRNA"

## ORIGIN

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 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-935-390A-23 (1-206) x AR237449 (1-1542)

QY 1 MetGluArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
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 QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40  
 DB 982 AATGGCTGCTGCATCGACATTTCTGGAGTGTGACGACACCCCACTGCCCGACGCC 1041  
 QY 41 SerAspGluAlaCysGluIleAspThrSerGlyPheAspGluLeuGlnArgIleHis 60  
 DB 1042 TCCGACGAGCTGCTGTGAAAATAACAGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1101  
 QY 61 PheProSerAspGlyHisCysValAspLeuProAspThrGlyLeuCysGlySer 80  
 DB 1102 TTCCCGAGTGCAGAGGCGACTCGGTGGACCTCCAGACACAGACTCTGCAAGGAGAGC 1161  
 QY 81 IleProArgTrpTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100  
 DB 1162 ATCCCGCTGTGTACTACACCCCTTCAGGACACTGCGCGCTTTTACCTATGTGT 1221  
 QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnCysLeuGluSerCysArgGly 120  
 DB 1222 TGTATGGCAACAGAACAACTTTGAGAGAGACAGACAGTGCCTCGAGTCTGTGCGGC 1281  
 QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140  
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 QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160  
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 QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180  
 DB 1402 GGTACTGCTTCTTCAGAACCCAGAGAGGACTTCCAGGACACCCACCCACCA 1461  
 QY 181 ProThrProAlaSerSerThrValSerThrGluAspThrGluHisLeuValTyrAsn 200  
 DB 1462 CCCACCCCTGCCAGTCTGCTCCACTACCGAGGACAGGACGACCTGCTGTATAC 1521  
 QY 201 HisThrThrArgProLeu 206  
 DB 1522 CACACCCCGGCCCTC 1539

## RESULT 6

BT007425  
 LOCUS BT007425 1542 bp mRNA linear PRI 13-MAY-2003  
 DEFINITION Homo sapiens serine protease inhibitor, Kunitz type 1 mRNA,  
 complete cds.  
 ACCESSION BT007425  
 VERSION BT007425.1 GI:30583688  
 KEYWORDS FLI CDNA.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 1542)  
 AUTHORS Kainine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,  
 Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,  
 Phelan,M. and Farmer,A.  
 TITLE Cloning of human full-length CDSs in BD Creator(TM) System Donor  
 vector  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1542)  
 AUTHORS Kainine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,  
 Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,  
 Phelan,M. and Farmer,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow  
 Circle, Palo Alto, CA 94303, USA  
 COMMENT This CDS clone is a part of a collection of human full length  
 expression clones generated by BD Biosciences Clontech and the  
 Harvard Institute of Proteomics. Each CDS has been cloned in two  
 forms: with and without stop-codon (to allow fusion with C-terminal  
 tag). The CDS has been directionally cloned using BD in-Fusion(TM)  
 cloning system between the Sali and HindIII sites of the pDNR-DUAL  
 vector. Additional sequences in the clone: 'ACC' after Sali site  
 and before 'ATG' to provide Kozak consensus sequence; 'GG' after  
 last codon and before HindIII site to maintain reading frame.  
 Clone distribution: <http://bioinfo.clontech.com/orfclones>.  
 FEATURES  
 source Location/Qualifiers  
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 /db\_xref="taxon:9606"  
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 ELQPDREGDAIACFLINCLYBQNFVCKPAPREGFINLYTRVYSYRLRTQGGGS  
 GIPKAWAGIDKQPELVKQVNDWRLRGDIDVVRKQDQVQVQLVGLGKGT  
 LPQLVTSSEHPDETANVTIVLTSTQTDYCLASNKVGRGCSPPRWYDTEQICK  
 SFVYGGCLGNKNYLRREECILACRGVQSPMERHPVCSGTQPTQPCNSGCCIDS  
 FLECDPTNPCEADSAACEKYTSGFDELQRIHPPSDKGHCVDLDTGLCKESIPIRY  
 YNPFSEHCARTYGGCYGNKNFEEQCLSCRGISKXQVFLAREIPIPTSGVEM  
 AVAFVLICIVVWVAILGYCFKQKDFHGHHPPTPASSTVSTTDEHLVYNH  
 TTRPL"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 4,72e-117 Length: 1542  
 Score: 1167.00 Matches: 206  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0  
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 Qy 1 MetGluArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
 Db 922 ATGCAAGAGGCCATCCAGTGTCTGTGGCACTGTGACGCCACCCAGTTCCTGTCGAC 981  
 Qy 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspSerThrProAsnCysProAspAla 40  
 Db 982 AATGGCTGCTGCATCGACAGTTCCTGTAGTGTGACGACACCCCACTGCCCGGACGCC 1041  
 Qy 41 SerAspGluAlaAlaCysGluLysfYrThrSerGlyPheAspGluLeuGlnArgIleHis 60

Db 1042 TCCGACGAGGCTGCTCTGTGAATAATACACGAGTGGCTTTTACGAGGCTCCAGCGCATCCAT 1101  
 Qy 61 PheProSerAspIysGlyHisCysValAspLeuProAspThrGlyLeuCysIysGluSer 80  
 Db 1102 TTCCCCAGTGTGACAAAGGGCACTGCTGTGGACTCTGCAGACACAGACTCTCTCAAGGAGGC 1161  
 Qy 81 IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100  
 Db 1162 ATCCGGGGCTGTGTACTACAAACCCCTTCAGCGAACACCTGCGCCCGCTTTACTATGGTGT 1221  
 Qy 101 CysTyrGlyAsnIysAsnAspPheGluGluGluGlnCysLeuGluSerCysAspGly 120  
 Db 1222 TGTATGTCACACAGAACACACTTTGAGAGAGAGACGACGAGTCTCTCGAGTCTTGTTCGGGC 1281  
 Qy 121 IleSerIysIysAspValPheGlyLeuArgGluIleProIleProSerThrGlySer 140  
 Db 1282 ATCTCCAGAGAGATGTGTGTGGCTTGGCGCGGGAATCCCATTCACGACACAGGCTCT 1341  
 Qy 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160  
 Db 1342 GTGAGAGGCTGTGCGAGGTTCCTGTGTCATCTGCATTGTGTGGTGTGGTGTGCTTTG 1401  
 Qy 161 GlyTyrCysPhePheIysAsnGlnArgIysAspPheHisGlyHisHisHisProPro 180  
 Db 1402 GGTACTGCTTCTTCAAGAACACAGAGAAAGGACTTCCACGACACACACACACACCA 1461  
 Qy 181 ProThrProIaSerSerThrValSerThrGluAspThrGluHisLeuValTyrAsn 200  
 Db 1462 CCCACCCCTGCCAGTCCACTGTCTCCATCCGAGGACACGGAGGACCTGGTCTTATAC 1521  
 Qy 201 HisThrThrArgProLeu 206  
 Db 1522 CACACACCGCGGCCCTC 1539  
 RESULT 7  
 LOCUS BT009882 1542 bp mRNA linear SYN 02-AUG-2003  
 DEFINITION Synthetic construct Homo sapiens serine protease inhibitor, Kunitz  
 type 1 mRNA, partial cds.  
 ACCESSION BT009882  
 VERSION BT009882.1 GI:32880106  
 KEYWORDS FLI CDNA.  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE 1 (bases 1 to 1542)  
 AUTHORS Kainine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,  
 Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,  
 Phelan,M. and Farmer,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-JUL-2003) BD Biosciences Clontech, 1020 East Meadow  
 Circle, Palo Alto, California 94303, USA  
 REFERENCE 2 (bases 1 to 1542)  
 AUTHORS Kainine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,  
 Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,  
 Phelan,M. and Farmer,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-AUG-2003) BD Biosciences Clontech, 1020 East Meadow  
 Circle, Palo Alto, California 94303, USA  
 COMMENT This CDS clone is a part of a collection of human full length  
 expression clones generated by BD Biosciences Clontech and the  
 Harvard Institute of Proteomics. Each CDS has been cloned in two  
 forms: with and without stop-codon (to allow fusion with C-terminal  
 tag). The CDS has been directionally cloned using BD in-Fusion(TM)  
 cloning system between the Sali and HindIII sites of the  
 pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after  
 Sali site and before 'ATG' to provide Kozak consensus sequence;  
 'GG' after last codon and before HindIII site to maintain reading  
 frame. Clone distribution: <http://bioinfo.clontech.com/orfclones>.  
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 source Location/Qualifiers  
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 /organism="synthetic construct"



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Score: 1167.00 Matches: 206
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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QY 101 CysTyrGlyAsnLysAsnAnpPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
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LOCUS ARI23705 1870 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 6 from patent US 6171790.
ACCESSION ARI23705
VERSION ARI23705.1 GI:14109066
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1870)
AUTHORS Hillman,J.L., Tang,Y.Tom., Lal,P., Corley,N.C., Guegler,K.J. and
Patterson,C.
TITLE Human protease associated proteins
JOURNAL Patent: US 6171790-A 6 09-JAN-2001;
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Db 620 AATGCTGCTGCTGAGAGTTCCTGAGTGTGACACACCCCAACTGCCCGCAGCC 679
QY 41 SerAspGluAlaAlaCysGluLeuGlyThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 680 TCCGACGAGGCTGCTGTGAAAATACACAGTGGCTTTCAGAGCTCCAGGCGATCCAT 739
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 740 TTCCCGAGTGCAGAGGCACTGCTGTGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 799
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QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
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LOCUS Human protease associated proteins.
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ACCESSION BD205506.1 GI:33015276
VERSION JP 2002513572-A/2.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1870)
AUTHORS Hillman,J.L., Tang,T.Y., Lal,P., Corley,N.C., Guegler,K.J. and
Patterson,C.
TITLE Human protease associated proteins
JOURNAL Patent: JP 2002513572-A 2 14-MAY-2002;
INCYTE PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002513572-A/2
PD 14-MAY-2002
PF 28-APR-1999 JP 2000547229
PR 01-MAY-1998 US 09/071709
PI JENNIFER L HILLMAN,TOM Y TANG,PREETI LAL,NEIL C CORLEY,KARL J
PI GUEGLER,
PI CHANDRA, PATTERSON
PC C12N15/09,A61K38/00,A61K45/00,A61P19/02,A61P35/00,A61P37/02,
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DEFINITION variant 2, mRNA (cDNA clone MGC:1726 IMAGE:295938), complete cds.
ACCESSION BC004140
VERSION BC004140.1 GI:13278722
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 2297)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
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Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
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Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalios,D.E.,
Scherer,A., Schein,J.E., Jones,S.J. and Marra,M.A.
GENERATION and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 2297)
Direct Submission
Strausberg,R.
TITLE
JOURNAL
MEDLINE
PUBMED
AUTHORS
TITLE
JOURNAL

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Submitted (01-VAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

REMARK  
COMMENT

USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapps-remail.nih.gov](mailto:cgapps-remail.nih.gov)  
Tissue Procurement: ARCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
contact: [amandusystemsbiology.org](mailto:amandusystemsbiology.org)  
Anup Madan, Jessica Fahey, Brin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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US-09-935-390A-23 (1-206) x BC004140 (1-2297)

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QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60  
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RESULT 11  
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DEFINITION Homo sapiens mRNA for hepatocyte growth factor activator inhibitor, complete cds.  
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VERSION AB000095.1 GI:2924600  
KEYWORDS hepatocyte growth factor activator inhibitor.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1 (sites)  
AUTHORS Shimomura,T., Denda,K., Kitamura,A., Kawaguchi,T., Kito,M., Kondo,J., Kagaya,S., Qin,L., Takata,H., Miyazawa,K. and Kitamura,N.  
TITLE Hepatocyte growth factor activator inhibitor, a novel Kunitz-type serine protease inhibitor  
J. Biol. Chem. 272 (10), 6370-6376 (1997)  
J. Biol. Chem. 272 (10), 6370-6376 (1997)  
MEDLINE 97197808  
PUBMED 9045658  
REFERENCE 2 (bases 1 to 2399)  
AUTHORS Denda,K.  
TITLE Direct Submission  
JOURNAL Submitted (24-DEC-1996) Kimitoshi Denda, Tokyo Institute of Technology, Department of Life Science, 4259 Nagatsuta, Midori-ku, Yokohama, Kanagawa 227, Japan (E-mail:kdenda@bio.titech.ac.jp, Tel:45-924-5702, Fax:45-924-5771)  
FEATURES Location/Qualifiers

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US-09-935-390a-23 (1-206) x AB000095 (1-2399)			
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DB	1097	ATGGAAGCGCGCATCCAGTGCTCTGCACCTCTCAGCCACCCAGCTTCGCTGCAGC	1156
QY	21	AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla	40
DB	1157	ATGCTCTCTGATCGACAGATTCTTGAGTGAGACACCCCACTGCCCCACGCC	1216
QY	41	SerAspGluAlaAlaCysGluIysTyrThrSerGlyPheAspGluLeuGlnArgIleHis	60
DB	1217	TCCGACGAGCTGCTGTGTAATAATACAGAGTGCTTTGACAGCTTCAGCGCATCCAT	1276
QY	61	PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysIysGluSer	80
DB	1277	TTCCCCAGTGACAAAGGCGCTGCTGGACCTGCCAGACACAGGACTCTGCAGGAGAGC	1336
QY	81	IleProArgTyrTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly	100
DB	1337	ATCCCGCGCTGTACTACAAACCCCTTCCAGCAACACTGCGCCCGCTTTACCTATGCTGT	1396
QY	101	CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly	120
DB	1397	TGTTATGGCAACAGAACAACTTTGAGGAGAGCAGCAGTGCCTCGAGTCTTGTGCGCGC	1456
QY	121	IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer	140
DB	1457	ATCTCCAGAGAGATGTGTTTGCTGAGCGGGAATCCCAATCCAGCAGCAGCTCT	1516
QY	141	ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu	160
DB	1517	GTGGAGATGCTGTGCGAGTGTCTCTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCT	1576
QY	161	GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro	180
DB	1577	GGTACTGCTCTTCTCAAGAACACAGAAAGGACTCCACGACACACACACACACCA	1636
QY	181	ProThrProAlaSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn	200
DB	1637	CCACCCCTGCCAGCTCCACTGCTCTCACTACCGAGACACGAGCAGCTGCTGTATAAC	1696
QY	201	HisThrThrArgProLeu	206

Db	1697	CACACACCGCGCCCTC	1714
RESULT 12			
LOCUS	BC018702		
DEFINITION	Homo sapiens serine protease inhibitor, Kunitz type 1, transcript variant 2, mRNA (CDNA clone MGC:15571 IMAGE:3140292), complete cds.		
ACCESSION	BC018702		
VERSION	BC018702.1	GI:17511685	
KEYWORDS	MGC		
SOURCE	Homo sapiens (human)		
ORGNISM	Homo sapiens		
REFERENCE	1. (bases 1 to 2486)		
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,K.H., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Haieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.D., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.R., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shvachenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Shen,S.D., Dicken,C.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E., Schmech,A., Schein,J.B., Jones,S.J. and Marra,M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
MEDLINE	22388257		
PUBMED	12477932		
AUTHORS	2. (bases 1 to 2486)		
TITLE	Strausberg,R.		
JOURNAL	Direct Submission		
REMARK	Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letitia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Cardice McLeavy, Steven Neas, Pawan Pandoh, Anna-Lilaea Prabhu, Parvaneh Saedi, Jacqueline Schein, Duane Smalish, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.		
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL plate: 22 Row: h Column: 7. Location/Qualifiers 1. .2486 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:15571 IMAGE:3140292"		



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Score: 1163.00 Matches: 205
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
DB: 9 Gaps: 0

US-09-935-390A-23 (1-206) x AX296715 (1-2370)

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QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
Db 1117 AATGGCTGTGTCATCCAGATTTCTCGAGTGTGACGACACCCCACTGCCCGACGCC 1176
QY 41 SerAspGluAlaAlaCysGluYsYrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 1177 TCCGACGAGGCTGCTGTGAANAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1236
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 1237 TTCCCGAGTGACAAAGGCGACTGCTGGACCTGCCAGACACAGGACTTGCAGGAGGC 1296
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 1297 ATCCCGCGCTGTACTCAACCCCTTCAGGAAACATCTGGCCCGCTTTACCTATGTTGT 1356
QY 101 CysTyrGlyAsnLysAsnLeuPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
Db 1357 TGTATTATGCAACAAAGAACAACTTTGAGGAAGACGACGAGTGGCTCGAGTCTTGTGCGGC 1416
QY 121 IleSerLysLysAspValPheGlyLeuArgGluLeuProIleProSerThrGlySer 140
Db 1417 ATCTCAAGAGGATGTGTTCGCTCATCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1476
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
Db 1477 GTGAGATGGCTGTCACAGTGTTCCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1536
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisProPro 180
Db 1537 GGTACTGCTCTCTCAAGAACACGAGAAAGGACTTCCAGGACACACACACACACACCA 1596
QY 181 ProThrProAlaSerThrValSerThrGluAspThrGluHisLeuValTyrAsn 200
Db 1597 CCCACCCCTGCCAGCTCCACTGCTCCACTACCGAGGACACGAGGACCTGGTCTATAAC 1656
QY 201 HisThrArgProLeu 206
Db 1657 CACACACCGCGCCCTC 1674

RESULT 14
AX077023 2482 bp DNA linear PAT 22-FEB-2001
LOCUS
DEFINITION Sequence 11 from Patent WO0105972.
ACCESSION AX077023
VERSION AX077023.1 GI:13121657
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
Location/Qualifiers
1. .2482

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Score: 2.26e-116 Length: 2482
Pred. No.: 1163.00 Matches: 205
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
DB: 6 Gaps: 0

US-09-935-390A-23 (1-206) x AX077023 (1-2482)

QY 1 MetGluArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 1157 ATGGAAGGCGCCATCCAGTGTCTCTGGCACCCTGTGAGCCACCCAGTTCGCTGCAGC 1216
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
Db 1217 AATGGCTGTGTCATCCAGATTTCTCGAGTGTGACGACACCCCACTGCCCGACGCC 1276
QY 41 SerAspGluAlaAlaCysGluYsYrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 1277 TCCGACGAGGCTGCTGTGAANAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1336
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 1337 TTCCCGAGTGACAAAGGCGACTGCTGGACCTGCCAGACACAGGACTTGCAGGAGGC 1396
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 1397 ATCCCGCGCTGTACTCAACCCCTTCAGGAAACATCTGGCCCGCTTTACCTATGTTGT 1456
QY 101 CysTyrGlyAsnLysAsnLeuPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
Db 1457 TGTATTATGCAACAAAGAACAACTTTGAGGAAGACGACGAGTGGCTCGAGTCTTGTGCGGC 1516
QY 121 IleSerLysLysAspValPheGlyLeuArgGluLeuProIleProSerThrGlySer 140
Db 1517 ATCTCAAGAGGATGTGTTCGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1576
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
Db 1577 GTGAGATGGCTGTCACAGTGTTCCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1636
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisProPro 180
Db 1637 GGTACTGCTCTCTCAAGAACACGAGAAAGGACTTCCAGGACACACACACACACCA 1696
QY 181 ProThrProAlaSerThrValSerThrGluAspThrGluHisLeuValTyrAsn 200
Db 1697 CCCACCCCTGCCAGCTCCACTGCTCCACTACCGAGGACACGAGGACCTGGTCTATAAC 1756
QY 201 HisThrArgProLeu 206
Db 1757 CACACACCGCGCCCTC 1774

RESULT 15
AX201332 2482 bp DNA linear PAT 30-AUG-2001
LOCUS
DEFINITION Sequence 11 from Patent WO0153486.
ACCESSION AX201332
VERSION AX201332.1 GI:15391158
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS

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Stone, D.M., Watanabe, C.K. and Wood, W.I.  
Compositions and methods for the treatment of tumour  
Patent: WO 0153486-A 11 26-JUL-2001;

TITLE  
JOURNAL

Genentech, Inc. (US)

FEATURES

source

1. 2482

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 2.26e-116 Length: 2482

Score: 1163.00 Matches: 205

Percent Similarity: 99.51% Conservative: 0

Best Local Similarity: 99.51% Mismatches: 1

Query Match: 99.66% Indels: 0

DB: 6 Gaps: 0

US-09-935-390A-23 (1-206) x AX201332 (1-2482)

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QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
DB 1157 ATGGAAGCGCCATCCAGTGTCTGTGGCAGCTGTGACCCACCCAGTTCGGTGCAGC 1216

QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
DB 1217 AATGCTGTGTCATGACAGTTTCCTGGAGTGTGACGACACCCCACTGCCCCGACGCC 1276

QY 41 SerAspGluAlaAlaCysGluLysTrpThrSerGlyPheAspGluLeuGlnArgIleHis 60
DB 1277 TCCGACGAGGCTGCTGTGAAATAACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1336

QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
DB 1337 TTCCCCAGTCAGAAAGGACACTGGCTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 1396

QY 81 IleProArgTrpTyrTrpAsnProPheSerGluHisCysAlaArgPheThrThrGlyGly 100
DB 1397 ATCCCGGCGCTGGTACTACACCCCTTCAGCGAACAACCTCGCCCGCTTTTACCTATGGTGGT 1456

QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
DB 1457 TGTATGACACACAGAAACAATTTGAGGAGAGGACGAGCTGCTCGACTCTGTGCGGCG 1516

QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
DB 1517 ATCTCCAGAGAGGATGTGTTGGCTGTGAGCGGGGAAATCCCAATTTCCAGACACAGGCTCT 1576

QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeu 160
DB 1577 GTGGAGATGGCTGTACAGTGTCTCTGATCTCTGATCTGATCTGATCTGATCTGATCTG 1636

QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisHisProPro 180
DB 1637 GGTACTGCTTCTTCAAGAACACAGAGAAAGAGACTTCCACGGACACACACACACACCA 1696

QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
DB 1697 CCCACCCCTGCGAGCTCCACTCTCTACTACCGAGGACACGAGGACCTGGTCTATTAAC 1756

QY 201 HisThrThrArgProLeu 206
DB 1757 CACACACCCCGCGCCCTC 1774

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Search completed: April 22, 2004, 09:32:11  
Job time : 3737 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2004, 10:14:05 ; Search time 65 Seconds  
(without alignments)  
999.950 Million cell updates/sec

Title: US-09-935-390A-23  
Perfect score: 206  
Sequence: 1 MERRHPVCSGTQPTQFRCS.....TGSTEDTSLVNHHTREL 206

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL\_25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phages:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	145	70.4	529	4 Q7Z7D2	Q7Z7D2 homo sapien
2	40	19.4	507	11 Q9D3K4	Q9D3K4 mus musculus
3	40	19.4	507	11 Q9D3J04	Q9D3J04 mus musculus
4	9	4.4	390	10 Q7XR48	Q7XR48 oryza sativ
5	8	3.9	250	10 Q8H2V9	Q8H2V9 oryza sativ
6	8	3.9	350	4 Q9NV85	Q9NV85 homo sapien
7	8	3.9	350	4 Q9H813	Q9H813 homo sapien
8	8	3.9	350	11 Q9CZV9	Q9CZV9 mus musculus
9	8	3.9	350	11 Q9D771	Q9D771 mus musculus
10	8	3.9	586	5 Q9V832	Q9V832 drosophila
11	8	3.9	597	6 Q9TVD1	Q9TVD1 bos tauri
12	8	3.9	758	16 Q8DFQ8	Q8DFQ8 vibrio vuln
13	8	3.9	758	16 Q87RD9	Q87RD9 vibrio para
14	8	3.9	759	16 Q99TL6	Q99TL6 staphylococ
15	8	3.9	826	4 O00420	O00420 homo sapien
16	8	3.9	846	16 Q8XUK5	Q8XUK5 ralstonia s

17	8	3.9	846	16 Q8XPV0	Q8XPV0 ralstonia s
18	8	3.9	1743	5 Q9XWXS	Q9XWXS caenorhabdi
19	7	3.4	62	5 Q26358	Q26358 onchocerca
20	7	3.4	78	11 Q9QY97	Q9QY97 rattus norv
21	7	3.4	102	5 Q9VUE1	Q9VUE1 drosophila
22	7	3.4	106	16 Q8NSZ6	Q8NSZ6 corynebacte
23	7	3.4	114	11 Q9CQH0	Q9CQH0 mus musculu
24	7	3.4	114	11 Q92382	Q92382 rattus norv
25	7	3.4	116	1 Q9UXM3	Q9UXM3 sulfolobus
26	7	3.4	116	12 Q69278	Q69278 equine herp
27	7	3.4	125	6 Q9N123	Q9N123 macaca fasc
28	7	3.4	132	5 Q9VQT9	Q9VQT9 drosophila
29	7	3.4	135	16 Q97H02	Q97H02 clostridium
30	7	3.4	136	5 Q86KR0	Q86KR0 dictyosteli
31	7	3.4	150	2 Q9FIP7	Q9FIP7 burkholderi
32	7	3.4	150	2 Q9ZF82	Q9ZF82 burkholderi
33	7	3.4	150	2 Q9LAN4	Q9LAN4 burkholderi
34	7	3.4	152	10 Q93738	Q93738 flaveria cr
35	7	3.4	159	3 O14146	O14146 schizosacch
36	7	3.4	162	10 Q39751	Q39751 flaveria pr
37	7	3.4	165	5 Q964Q0	Q964Q0 ixodes scap
38	7	3.4	173	17 Q9YC33	Q9YC33 aeropyrum p
39	7	3.4	178	17 Q9HI83	Q9HI83 thermoplasm
40	7	3.4	193	10 Q84ZF1	Q84ZF1 oryza sativ
41	7	3.4	193	16 Q8NN01	Q8NN01 corynebacte
42	7	3.4	195	2 Q9ZHW7	Q9ZHW7 bruceella me
43	7	3.4	202	16 Q89582	Q89582 mycobacteri
44	7	3.4	203	5 Q95FM3	Q95FM3 nippostro
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ALIGNMENTS

RESULT 1

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ID Q7Z7D2;			
AC Q7Z7D2;			
DT 01-OCT-2003 (TREMELrel. 25, Created)			
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)			
DE 01-OCT-2003 (TREMELrel. 25, Last annotation update)			
DE Hepatocyte growth factor activator inhibitor 1B.			
GN HAI1.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Kirchhofer D., Peek M., Li W., Stamos J., Eigenbrot C., Moran P.;			
RA Kadhodayan S., Elliott J.M., Corpuz R.T., Lazarus R.A., Moran P.;			
RT "Tissue-expression, protease-specificity and Kunitz domain functions			
RT of HAI-1B, a new splice variant of hepatocyte growth factor activator			
RT inhibitor-1."			
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
RN [2]			
RP SEQUENCE FROM N.A.			
RA Yuan J., Moran P.;			
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.			
DR EMBL; AY296715; AAP44001.1; ..			
SQ SEQUENCE 529 AA; 58428 MW; B40F286C36D23437 CRC64;			

Query Match 70.4%; Score 145; DB 4; Length 529;  
Best Local Similarity 100.0%; Pred. No. 4.6e-150;  
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	324 MERRHPVCSGTQPTQFRCSGCCISDLECDTFCNCPDASDEAAACEKYTSFDSLQRIH 383		
QY	61 FPSDKGHCVLDPDTGLCKESIPRWYINPFSHCARFTYGGYGNKNFNFEEOQCLESCKG 120		
Db	384 FPSDKGHCVLDPDTGLCKESIPRWYINPFSHCARFTYGGYGNKNFNFEEOQCLESCKG 443		



Qy 121 ISKDVFGRLRRRIPITGSGVEMAV 145  
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 Db 444 ISKDVFGRLRRRIPITGSGVEMAV 468

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Q9D3K4 PRELIMINARY; PRT; 507 AA.  
 AC Q9D3K4  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
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 GN SPINT1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
 RA Strausberg R.;  
 RA SPINT1.  
 RA Mus musculus (Mouse).  
 RA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 RA Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RA NCBI\_TaxID=10090;  
 RA [1]  
 RA SEQUENCE FROM N.A.  
 RA STRAIN=CS7BL/6J; TISSUE=Head;  
 RA MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Macsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boiffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gueniche S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RA "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 403:685-690(2001).  
 DR EMBL; AK017342; BAB30697.1; -.  
 DR HSSP; P05067; 1CA0.  
 DR MGD; MGI:1338033; Spint1.  
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR InterPro; IPR002172; LDL\_receptor\_A.  
 DR Pfam; PF00014; Kunitz\_BPTI; 2.  
 DR Pfam; PF00057; ldl\_recept\_a; 1.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR ProDom; PD000222; Kunitz\_BPTI; 2.  
 DR SMART; SM00131; KU; 2.  
 DR SMART; SM00192; LDLA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 2.  
 DR PROSITE; PS02279; BPTI\_KUNITZ\_2; 2.  
 DR PROSITE; PS02209; LDLRA\_1; 1.  
 DR PROSITE; PS00068; LDLRA\_2; 1.  
 DR PROSITE; PS00068; LDLRA\_2; 1.  
 KW Protease inhibitor; Serine protease inhibitor.  
 SQ SEQUENCE 507 AA; 56571 MW; 98E0A29B7056D72D CRC64;

Query Match 19.4%; Score 40; DB 11; Length 507;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-35;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 CARFTYGGYGNKNFEEQQCLSCRGISKKDVFLGRRE 132  
 |||||

Db 394 CARFTYGGYGNKNFEEQQCLSCRGISKKDVFLGRRE 433

## RESULT 3

Q99J04

Q99J04 PRELIMINARY; PRT; 507 AA.  
 AC Q99J04  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Serine protease inhibitor, kunitz type 1 (Spint1 protein).  
 GN SPINT1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
 RA Strausberg R.;  
 RA SPINT1.  
 RA Mus musculus (Mouse).  
 RA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 RA Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RA NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP STRAIN=FVB/N-3; TISSUE=Breast tumor;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.P., Bhat N.K.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Murty D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skaleck U., Smailus D.E., Schnerch A., Schein J.S.,  
 RA Jones S.J., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RA and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N-3; TISSUE=Breast tumor;  
 RA Strausberg R.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC005769; AAH05769.1; -.  
 DR EMBL; BC053341; AAH53341.1; -.  
 DR HSSP; P05067; 1CA0.  
 DR MGD; MGI:1338033; Spint1.  
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.  
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR InterPro; IPR002172; LDL\_receptor\_A.  
 DR Pfam; PF00014; Kunitz\_BPTI; 2.  
 DR Pfam; PF00057; ldl\_recept\_a; 1.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR ProDom; PD000222; Kunitz\_BPTI; 2.  
 DR SMART; SM00131; KU; 2.  
 DR SMART; SM00192; LDLA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 2.  
 DR PROSITE; PS02279; BPTI\_KUNITZ\_2; 2.  
 DR PROSITE; PS02209; LDLRA\_1; 1.  
 DR PROSITE; PS00068; LDLRA\_2; 1.  
 DR PROSITE; PS00068; LDLRA\_2; 1.  
 KW Protease inhibitor; Serine protease inhibitor.  
 SQ SEQUENCE 507 AA; 56590 MW; F7F9CCT2693D1F8D CRC64;

Query Match 19.4%; Score 40; DB 11; Length 507;

Best Local Similarity 100.0%; Pred. No. 6.8e-35;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 CARFTYGGYGNKNFEEQQCLSCRGISKKDVFLGRRE 132

Db 394 CARFTYGGYGNKNFEEQQCLSCRGISKKDVFLGRRE 433

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RESULT 4
Q7XR48      PRELIMINARY;      PRT;      390 AA.
ID AC Q7XR48
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DE OSUNBA0043A12.37 protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.P., Tu Y.F.,
RA Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y.,
RA Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W.,
RA Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu P.H., Han B., Feng Q.,
RA Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z.,
RA Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H.,
RA Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,
RA Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M.,
RA Zhang R.Q., Guan J.P., Hong G.F.;
RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL606619; CAB02832.1; -
SQ SEQUENCE 390 AA; 41437 MW; 8B9D170A7808F1FE CRC64;

Query Match      4.4%; Score 9; DB 10; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 HGHHRHPPP 181
DB 247 HGHHRHPPP 255

RESULT 5
Q8H2V9      PRELIMINARY;      PRT;      250 AA.
ID AC Q8H2V9
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DE OSUNBB0011E04.11 protein.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, BAC
clone:OSUNBB0011E04.11";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005443; BAC22566.1; -
SQ SEQUENCE 250 AA; 27639 MW; 60DA333BAD5822FF CRC64;

Query Match      3.9%; Score 8; DB 10; Length 250;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 PPPTPASS 186
DB 168 PPPTPASS 175

RESULT 6
Q9NV85      PRELIMINARY;      PRT;      350 AA.
ID AC Q9NV85
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DE OSUNBA0043A12.37 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isozaki T., Ota T., Hayaashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraka S., Ishii S., Kawai Y.,
RA Saito K., Yamamoto Y., Wakamatsu A., Nakamura Y., Nagahari K.,
RA Masuho Y., Kanehori K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK001736; BAA91870.1; -
KW Hypothetical protein.
SQ SEQUENCE 350 AA; 39956 MW; D7B5875C34C9398C CRC64;

Query Match      3.9%; Score 8; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 MAVAVFLV 150
DB 78 MAVAVFLV 85

RESULT 7
Q9H813      PRELIMINARY;      PRT;      350 AA.
ID AC Q9H813
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DE OSUNBA0043A12.37 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isozaki T., Ota T., Hayaashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M.,
RA Wagatsuma M., Hosoiri T., Raku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwavanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK024066; BAB14810.1; -
DR EMBL; BC006320; AA06320.1; -
KW Hypothetical protein.
SQ SEQUENCE 350 AA; 40043 MW; 5F68ACA21DDD0674 CRC64;

Query Match      3.9%; Score 8; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 MAVAVFLV 150
DB 78 MAVAVFLV 85

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RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamei M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection."
RA Nature 409:685-690(2001).
RA [2]
RA SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Embryo;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamei M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection."
RA Nature 409:685-690(2001).
RA EMBL; AK012107; BAB28038.1; -
RA MGD; MGI:1914200; 2310028N02Rik.
SQ SEQUENCE 350 AA; 40285 MW; 12FD43319660775B CRC64;

Query Match 3.9%; Score 8; DB 11; Length 350;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 MAVAVFLV 150
DB 78 MAVAVFLV 85
|||||
PRT; 350 AA.

RESULT 9
Q9D771 PRELIMINARY; PRT; 350 AA.
ID Q9D771
AC Q9D771
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 2310028N02Rik protein (Hypothetical protein).
GN 2310028N02Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamei M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection."
RA Nature 409:685-690(2001).
RA EMBL; AK012107; BAB28038.1; -
RA MGD; MGI:1914200; 2310028N02Rik.
SQ SEQUENCE 350 AA; 40285 MW; 12FD43319660775B CRC64;

Query Match 3.9%; Score 8; DB 11; Length 350;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 MAVAVFLV 150
DB 78 MAVAVFLV 85
|||||
PRT; 350 AA.

RESULT 9
Q9D771 PRELIMINARY; PRT; 350 AA.
ID Q9D771
AC Q9D771
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 2310028N02Rik protein (Hypothetical protein).
GN 2310028N02Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamei M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection."
RA Nature 409:685-690(2001).
RA EMBL; AK012107; BAB28038.1; -
RA MGD; MGI:1914200; 2310028N02Rik.
SQ SEQUENCE 350 AA; 40285 MW; 12FD43319660775B CRC64;

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RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamei M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection."
RA Nature 409:685-690(2001).
RA [2]
RA SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Retina, Spinal cord, and Testis;
RA MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RT Nature 420:563-573(2002).
RL EMBL; AK009526; BAB28340.1; -
DR EMBL; BC027151; AAH27151.1; -
DR EMBL; AK031270; BAC27330.1; -
DR EMBL; AK044482; BAC31946.1; -
DR EMBL; AK049641; BAC33853.1; -
DR MGD; MGI:1914200; 2310028N02Rik.
KW Hypothetical protein.
SQ SEQUENCE 350 AA; 40178 MW; 3EE2CFBE929AB003 CRC64;

Query Match 3.9%; Score 8; DB 11; Length 350;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 MAVAVFLV 150
DB 78 MAVAVFLV 85
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PRT; 586 AA.

RESULT 10
Q9VEG2 PRELIMINARY; PRT; 586 AA.
ID Q9VEG2
AC Q9VEG2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG16766 protein.
GN CG16766.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamei M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection."
RA Nature 409:685-690(2001).
RA [2]
RA SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Embryo;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamei M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection."
RA Nature 409:685-690(2001).
RA EMBL; AK012107; BAB28038.1; -
RA MGD; MGI:1914200; 2310028N02Rik.
SQ SEQUENCE 350 AA; 40285 MW; 12FD43319660775B CRC64;

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Q8DF08  
ID Q8DF08 PRELIMINARY; PRT; 758 AA.  
AC Q8DF08  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Fe2+ transport system protein B.  
GN VW10148.  
OS Vibrio vulnificus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
CX NCBI\_TaxID=672;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CMCP6;  
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,  
RA Choy H.E.;  
RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.";  
RL Submitted (DSC-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB016797; AAC08686.1; -.  
DR GO; GO:0015020; C:membrane; IEA.  
DR GO; GO:0015093; F:ferrous iron transporter activity; IEA.  
DR GO; GO:0015684; P:ferrous iron transport; IEA.  
DR InterPro; IPR004373; FeoB.  
DR InterPro; IPR006073; GTP1\_OBG.  
DR Pfam; PF02421; FeoB; 1.  
DR PRINTS; PR00326; GTP1\_OBG.  
DR TIGRFAMs; TIGR00437; feoB; 1.  
DR TIGRFAMs; TIGR00231; small\_GTP; 1.  
KW Complete proteome.  
SQ SEQUENCE 758 AA; 82450 MW; 3ABE990778B6A57D CRC64;  
Query Match 3.9%; Score 8; DB 16; Length 758;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 153 IVVVVAIL 160  
Db 516 IVVVVAIL 523

Q87RD9  
ID Q87RD9 PRELIMINARY; PRT; 758 AA.  
AC Q87RD9  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Ferrous iron transport protein B.  
GN VP0858.  
OS Vibrio parahaemolyticus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
CX NCBI\_TaxID=670;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RIMD 2210633 / Serotype O3:K6;  
RX MEDLINE=22508454; PubMed=12620739;  
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,  
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,  
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;  
RT "Genome sequence of *Vibrio parahaemolyticus*: a pathogenic mechanism distinct from that of *V. cholerae*.";  
RL Lancet 361:743-749 (2003).  
DR EMBL; AP005075; BACS9121.1; -.  
DR GO; GO:0015020; C:membrane; IEA.  
DR GO; GO:0015093; F:ferrous iron transporter activity; IEA.  
DR GO; GO:0015684; P:ferrous iron transport; IEA.  
DR InterPro; IPR003373; FeoB.  
DR InterPro; IPR006073; GTP1\_OBG.  
DR Pfam; PF02421; FeoB; 1.  
DR PRINTS; PR00326; GTP1\_OBG.

KW Complete proteome.  
SQ SEQUENCE 758 AA; 82555 MW; BEB6E07BCB8663D CRC64;  
Query Match 3.9%; Score 8; DB 16; Length 758;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 153 IVVVVAIL 160  
Db 516 IVVVVAIL 523

RESULT 14  
Q99TL6  
ID Q99TL6 PRELIMINARY; PRT; 759 AA.  
AC Q99TL6  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Protein-export membrane protein SecDF.  
GN SECDF OR SAV1637 OR SAL463 OR MW1587.  
OS *Staphylococcus aureus* (strain Mu50 / ATCC 700699),  
OS *Staphylococcus aureus* (strain N115), and  
OS *Staphylococcus aureus* (strain MW2).  
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.  
CX NCBI\_TaxID=158878, 158879, 196620;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MU50, and N315;  
RX MEDLINE=21311952; PubMed=11418146;  
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,  
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,  
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,  
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,  
RA Sekinezu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,  
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,  
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;  
RT "Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.";  
RL Lancet 357:1225-1240 (2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MW2;  
RX MEDLINE=22040717; PubMed=12044378;  
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,  
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,  
RA Yamamoto K., Hiramatsu K.;  
RT "Genome and virulence determinants of high virulence community-acquired MRSA.";  
RL Lancet 359:1819-1827 (2002).  
DR EMBL; AP003363; BAB57799.1; -.  
DR EMBL; AP003134; BAB42729.1; -.  
DR EMBL; AF004827; BAB95452.1; -.  
DR PIR; D89946; D89946.  
DR GO; GO:0019866; C:inner membrane; IEA.  
DR GO; GO:0015627; C:type II protein secretion system complex; IEA.  
DR GO; GO:0015450; P:protein translocase activity; IEA.  
DR GO; GO:0006886; P:intracellular protein transport; IEA.  
DR GO; GO:0015628; P:type II protein (Sec) secretion system; IEA.  
DR InterPro; IPR005791; SecD.  
DR InterPro; IPR003335; SecD\_SecF.  
DR Pfam; PF02355; SecD\_SecF; 1.  
DR PRINTS; PR01755; SECDFRNLCASE.  
DR TIGRFAMs; TIGR00916; 2A0604801; 2.  
DR TIGRFAMs; TIGR01129; secD; 1.  
KW Complete proteome.  
SQ SEQUENCE 759 AA; 84253 MW; 7E6B8BAC0D24BF47 CRC64;  
Query Match 3.9%; Score 8; DB 16; Length 759;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 153 IVVVVAIL 160

Db 688 IUVVAIL 695

RESULT 15  
O00420 PRELIMINARY; PRT; 826 AA.  
AC O00420  
DT 01-JUL-1997 (T-EMBLrel. 04, Created)  
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
DE E19541.1 (Fragment)  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lamerdin J.E., McCreedy P.M., Adamson A.A., Burkhardt-Schultz K.,  
RA Garcia E., Kyle A., Ramirez M., Stilwagen S., Ganes J., Danganan L.,  
RA Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,  
RA Carrano A.V.;  
RT "Sequence analysis of a 1 Mb region in human 19q13.1.";  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U95090; AAB80768.1; -;  
DR Genes; HGNC:17325; PRODH2.  
DR GO; GO:0004657; F:proline dehydrogenase activity; IEA.  
DR GO; GO:0004289; F:subtilase activity; IEA.  
DR GO; GO:0006537; P:glutamate biosynthesis; IEA.  
DR GO; GO:0006562; P:proline catabolism; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR002029; Peptidase\_S8.  
DR InterPro; IPR002872; Pro\_dh.  
DR Pfam; PF01619; Pro\_dh; 1.  
DR PROSITE; PS00138; SUBTILASE\_SER; 1.  
FT NON\_TER 1  
SQ SEQUENCE 826 AA; 90814 MW; 25CED0CB6970072E CRC64;

Query Match 3.9%; Score 8; DB 4; Length 826;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 185 SSTVSTTE 192  
Db 74 SSTVSTTE 81

Search completed: April 22, 2004, 10:25:16  
Job time : 68 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 22, 2004, 09:32:14 ; Search time 18 Seconds  
(without alignments)  
595.914 Million cell updates/sec

Title: US-09-935-390A-23

Perfect score: 206

Sequence: 1 MERRHPVCSTQPTQFRCS.....TWSTIEDTEHLYNHTTLP 206

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	100.0	513	1 SPT1_HUMAN	Q43278 homo sapien
2	40	19.4	507	1 SPT1_MOUSE	Q9R097 mus musculus
3	11	5.3	4660	1 LRP2_RAT	P98158 rattus norv
4	8	3.9	610	1 DPO1_BOVIN	F15101 bos taurus
5	8	3.9	1241	1 NPHN_HUMAN	O60500 homo sapien
6	7	3.4	90	1 Y585_ARCFU	O29670 archaeglob
7	7	3.4	114	1 MA17_HUMAN	Q13113 homo sapien
8	7	3.4	147	1 RZPR_BCOLI	P77551 escherichia
9	7	3.4	242	1 APL_IACLC	Q48630 lactococcus
10	7	3.4	354	1 CAHG_HUMAN	Q43570 homo sapien
11	7	3.4	387	1 QIN_AVIS3	P56260 avian sarco
12	7	3.4	436	1 BRNQ_HAEIN	P71345 haemophilus
13	7	3.4	451	1 FXGB_CHICK	Q90964 gallus gall
14	7	3.4	469	1 FXGB_HUMAN	P55316 homo sapien
15	7	3.4	477	1 FXGB_HUMAN	P55315 homo sapien
16	7	3.4	480	1 FXGB_RAT	Q0939 rattus norv
17	7	3.4	481	1 FXGB_MOUSE	Q60957 mus musculus
18	7	3.4	482	1 K6B2_HUMAN	Q9UB50 h ribosomal
19	7	3.4	485	1 K6B2_MOUSE	Q9Z1M4 mus musculus
20	7	3.4	502	1 K6B1_HUMAN	P23443 homo sapien
21	7	3.4	502	1 K6B1_RAT	P21425 rattus norv
22	7	3.4	510	1 HVAP_MACFA	P38568 macaca fasc
23	7	3.4	671	1 NCPR_MUSDO	Q07994 musca domes
24	7	3.4	672	1 SL52_HUMAN	P31639 homo sapien
25	7	3.4	902	1 NFC4_HUMAN	Q14934 homo sapien
26	7	3.4	950	1 KCH6_RAT	O54853 rattus norv
27	7	3.4	994	1 KCH6_HUMAN	Q9H252 homo sapien
28	7	3.4	994	1 PPOL_DROME	P35875 drosophila
29	7	3.4	1033	1 ACAC_ARATH	Q91777 arabidopsis
30	7	3.4	1158	1 KCH2_CANPA	Q9TSZ3 canis fami
31	7	3.4	1159	1 KCH2_HUMAN	Q12803 homo sapien
32	7	3.4	1161	1 KCH2_RABIT	Q8WY2 oryctolagus
33	7	3.4	1162	1 KCH2_MOUSE	O35219 mus musculus

#### ALIGNMENTS

RESULT 1				
SPT1_HUMAN				
ID	SPT1_HUMAN	STANDARD;	PRT;	513 AA.
AC	Q43278;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Kunitz-type protease inhibitor 1 precursor (Hepatocyte growth factor activator inhibitor type 1) (HAI-1).			
GN	SPINT1 OR HAI1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97197808; PubMed=9045658;			
RA	Shimomura T., Denda K., Kitamura A., Kawaguchi T., Kito M., Kondo J., Kagaya S., Qin L., Takata H., Miyazawa K., Kitamura N.;			
RT	"Hepatocyte growth factor activator inhibitor, a novel Kunitz-type serine protease inhibitor."			
RL	J. Biol. Chem. 272:6370-6376(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Colon, and Placenta;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C., Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heltón B., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson R.M., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzyzinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[3]			
RP	PARTIAL SEQUENCE, AND CHARACTERIZATION.			
RC	TISSUE=Milk;			
RX	MEDLINE=99303582; PubMed=10373425;			
RA	Lin C.Y., Anders J., Johnson M., Dickson R.B.;			
RT	"Purification and characterization of a complex containing matrilysin and a Kunitz-type serine protease inhibitor from human milk."			
RL	J. Biol. Chem. 274:18237-18242(1999).			
CC	!- FUNCTION: Inhibitor of HGF activator. Also acts as an inhibitor of matrilysin (ST14).			

O0962 rattus norv  
P33485 pseudorabie  
O00555 homo sapien  
P22052 bovine coro  
P26227 manduca sex  
P81547 anthopleura  
P00976 bos taurus  
Q9M4V4 mesostigma  
Q8T0W0 pimla hypo  
P56323 chlorella v  
P81060 penaeus van  
Q963d9 penaeus van

CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DOMAIN: This inhibitor contains two inhibitory domains.  
 CC -1- SIMILARITY: Contains 1 LDL-receptor class A domain.  
 CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC -----  
 DR EMBL; AB000095; BAA25014.1; --  
 DR EMBL; BC004140; AAH04140.1; --  
 DR EMBL; BC018702; AAH18702.1; --  
 DR HSSP; P31713; 1SHP.  
 DR -----  
 DR MIN; 605123; --  
 DR GO; GO:0005576; C:extracellular; TAS.  
 DR GO; GO:0005624; C:membrane fraction; TAS.  
 DR GO; GO:0004867; F:serine protease inhibitor activity; TAS.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR Pfam; PF00014; Kunitz\_BPTI; 2.  
 DR PRINTS; PR00759; lcl\_recept\_a; 1.  
 DR PRODOM; PD000222; Kunitz\_BPTI; 2.  
 DR SMART; SM00131; KU; 2.  
 DR SMART; SM00132; LDLa; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 2.  
 DR PROSITE; PS02079; BPTI\_KUNITZ\_2; 2.  
 DR PROSITE; PS01209; LDLRA\_1; 1.  
 DR PROSITE; PS00068; LDLRA\_2; 1.  
 KW Serine protease inhibitor; Repeat; Glycoprotein; Signal.  
 FT SIGNAL 1 35 KUNITZ-TYPE PROTEASE INHIBITOR 1.  
 FT CHAIN 36 513 BPTI/KUNITZ INHIBITOR 1.  
 FT DOMAIN 250 300 LDL-RECEPTOR CLASS A.  
 FT DOMAIN 318 354 BPTI/KUNITZ INHIBITOR 2.  
 FT DOMAIN 375 425 BY SIMILARITY.  
 FT DISULFID 250 300 BY SIMILARITY.  
 FT DISULFID 259 283 BY SIMILARITY.  
 FT DISULFID 275 296 BY SIMILARITY.  
 FT ACT\_SITE 260 261 REACTIVE BOND (BY SIMILARITY).  
 FT DISULFID 375 425 BY SIMILARITY.  
 FT DISULFID 384 408 BY SIMILARITY.  
 FT DISULFID 400 421 BY SIMILARITY.  
 FT ACT\_SITE 385 386 REACTIVE BOND (BY SIMILARITY).  
 FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 507 507 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 513 AA; 56985 MW; D6E09F3A5885CDDD CRC64;  
 Query Match 100.0%; Score 206; DB 1; Length 513;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-215;  
 Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MERRHPVCGTCQPTQPCNSGCCIDSPLECDTPNCPDASDEACAKYTSQPELQRIH 60  
 DB 308 MERRHPVCGTCQPTQPCNSGCCIDSPLECDTPNCPDASDEACAKYTSQPELQRIH 367  
 QY 61 FPSDKGHCVLDPTGLCKESIPRWYINPFSEHCARFTYGGCYGNKNFEEBQQCLSCRG 120  
 DB 368 FPSDKGHCVLDPTGLCKESIPRWYINPFSEHCARFTYGGCYGNKNFEEBQQCLSCRG 427  
 QY 121 ISKDVFLGRREIPITPSGVSVMVAVPLVTCIVVVAIIQYCFKQKQDPFGHHHPH 180  
 DB 428 ISKDVFLGRREIPITPSGVSVMVAVPLVTCIVVVAIIQYCFKQKQDPFGHHHPH 487  
 QY 191 PTPASSTVSTTDEHLVYNNHTPL 206  
 DB 488 PTPASSTVSTTDEHLVYNNHTPL 513

RESULT 2  
 SPTI\_MOUSE STANDARD; PRT; 507 AA.  
 ID SPTI\_MOUSE  
 AC Q9R097;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Kunitz-type protease inhibitor 1 precursor (Hepatocyte growth factor  
 DE activator inhibitor type 1) (HAI-1).  
 GN SPINT1 OR HAI1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALE/c;  
 RX MEDLINE=2129055; PubMed=11406276;  
 RA Itoh H., Kataoka H., Meng J.Y., Hamasuna R., Kitamura N., Koono M.;  
 RT "Mouse hepatocyte growth factor activator inhibitor type 1 (HAI-1).  
 RT and type 2 (HAI-2)/placental bikunin genes and their promoters.";  
 RL Biochim. Biophys. Acta 1519:92-95(2001).  
 CC -1- FUNCTION: Inhibitor of HGF activator (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -1- DOMAIN: This inhibitor contains two inhibitory domains.  
 CC -1- SIMILARITY: Contains 1 LDL-receptor class A domain.  
 CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.  
 CC -----  
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 CC -----  
 CC EMBL; AF099018; AAF02490.1; --  
 CC HSSP; P05067; 1CAO.  
 CC MGD; MGI:1338033; Spint1.  
 CC InterPro; IPR002223; Kunitz\_BPTI.  
 CC InterPro; IPR002172; LDL\_receptor\_A.  
 CC Pfam; PF00014; Kunitz\_BPTI; 2.  
 CC Pfam; PF00057; lcl\_recept\_a; 1.  
 CC PRINTS; PR00759; BASICPTASE.  
 CC PRODOM; PD000222; Kunitz\_BPTI; 2.  
 CC SMART; SM00131; KU; 2.  
 CC SMART; SM00132; LDLa; 1.  
 CC PROSITE; PS00280; BPTI\_KUNITZ\_1; 2.  
 CC PROSITE; PS02079; BPTI\_KUNITZ\_2; 2.  
 CC PROSITE; PS01209; LDLRA\_1; 1.  
 CC PROSITE; PS00068; LDLRA\_2; 1.  
 KW Serine protease inhibitor; Repeat; Glycoprotein; Signal.  
 FT SIGNAL 1 29 POTENTIAL.  
 FT CHAIN 30 507 KUNITZ-TYPE PROTEASE INHIBITOR 1.  
 FT DOMAIN 244 294 BPTI/KUNITZ INHIBITOR 1.  
 FT DOMAIN 312 348 LDL-RECEPTOR CLASS A.  
 FT DOMAIN 369 419 BPTI/KUNITZ INHIBITOR 2.  
 FT DISULFID 244 294 BY SIMILARITY.  
 FT DISULFID 253 277 BY SIMILARITY.  
 FT DISULFID 269 290 BY SIMILARITY.  
 FT ACT\_SITE 254 255 REACTIVE BOND (BY SIMILARITY).  
 FT DISULFID 369 419 BY SIMILARITY.  
 FT DISULFID 378 402 BY SIMILARITY.  
 FT DISULFID 394 415 BY SIMILARITY.  
 FT ACT\_SITE 379 380 REACTIVE BOND (BY SIMILARITY).  
 FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 501 501 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 507 AA; 56676 MW; 20CB5D8DCEP46AA7 CRC64;  
 Query Match 19.4%; Score 40; DB 1; Length 507;  
 Best Local Similarity 100.0%; Pred. No. 3e-35;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 93 CARFTYGGCYGNKNNFEEQQCLSCSGSKGVFLGRRE 132  
 Db |||||||  
 394 CARFTYGGCYGNKNNFEEQQCLSCSGSKGVFLGRRE 433

## RESULT 3

LRP2\_RAT STANDARD; PRT; 4660 AA.  
 AC P98158;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Low-density lipoprotein receptor-related protein 2 precursor (Megalin)  
 DE (glycoprotein 330) (gp330).  
 GN LRP2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;  
 RX MEDLINE=95024033; PubMed=7937880;  
 RA Saito A., Pietromonaco S., Loo A.K.C., Farquhar M.G.;  
 RT "Complete cloning and sequencing of rat gp330/megalin," a  
 RT distinctive member of the low density lipoprotein receptor gene  
 RT family.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9725-9729(1994).  
 RN [2]  
 RP FUNCTION.  
 RX MEDLINE=95386696; PubMed=7544804;  
 RA Moestrup S.K., Cui S., Vorum H., Bregengaard C., Bjorn S.B.,  
 RA Norris K., Gliemann J., Christensen B.I.;  
 RT "Evidence that epithelial glycoprotein 330/megalin mediates uptake of  
 RT polybasic drugs.";  
 RL J. Clin. Invest. 96:1404-1413(1995).  
 RN [3]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=94172242; PubMed=7510321;  
 RA Zheng G., Bachinsky D.R., Stamenkovic I., Strickland D.K., Brown D.,  
 RA Andres G., McCluskey R.T.;  
 RT "Organ distribution in rats of two members of the low-density  
 RT lipoprotein receptor gene family, gp330 and LRP/alpa 2MR, and the  
 RT receptor-associated protein (RAP).";  
 RL J. Histochem. Cytochem. 42:531-542(1994).  
 CC -!- FUNCTION: Binds plasminogen, extracellular matrix components,  
 CC plasminogen activator-plasminogen activator inhibitor type I,  
 CC complex, apolipoprotein B-enriched beta-VLDL, lipoprotein lipase,  
 CC lactoferrin, clusterin and calcium.  
 CC -!- FUNCTION: Receptor-mediated uptake of polybasic drugs such as  
 CC aprotinin, aminoglycosides and polymyxin B.  
 CC -!- SUBUNIT: Forms a multimeric complex together with a receptor-  
 CC associated protein (RAP). Binds to ankyrin-repeat family A protein  
 CC 2 (ANKRA2) (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Expressed in  
 CC clathrin-coated pits; a soluble form is possibly derived by  
 CC cleavage at the cell surface.  
 CC -!- TISSUE SPECIFICITY: Epithelial cells of kidney glomerulus and  
 CC proximal tubule, lung, epididymis, yolk sac, among others.  
 CC -!- SIMILARITY: Contains 36 LDL-receptor class A domains.  
 CC -!- SIMILARITY: Contains 37 LDL-receptor class B domains.  
 CC -!- SIMILARITY: Contains 17 EGF-like domains.  
 CC -----  
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 CC -----  
 CC EMBL; L34049; AAA51369.1; -.

PIR; T42737; T42737.  
 DR HSP; Q07954; 1CR8.  
 DR GlycoSuiteDB; P98158;  
 DR InterPro: IPR00152; Asx\_hydroxyl\_s.  
 DR InterPro: IPR001981; EGF\_Ca.  
 DR InterPro: IPR006209; EGF\_like.  
 DR InterPro: IPR002172; LDL\_receptor\_A.  
 DR InterPro: IPR000033; Ldl\_receptor\_rep.  
 DR Pfam: PF00008; EGF; 9.  
 DR Pfam: PF00057; ldl\_recept\_a; 36.  
 DR Pfam: PF00058; ldl\_recept\_b; 33.  
 DR PRINTS: PR00261; LDLRECEPTOR.  
 DR SMART: SM00179; EGF\_CA; 3.  
 DR SMART: SM00192; LDLA; 36.  
 DR SMART: SM00135; LY; 34.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 4.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; 8.  
 DR PROSITE: PS00026; EGF\_3; 8.  
 DR PROSITE: PS01187; EGF\_CA; 3.  
 DR PROSITE: PS01209; LDLRA\_1; 31.  
 DR PROSITE: PS00068; LDLRA\_2; 36.  
 KW Glycoprotein; Repeat; Endocytosis; Coated pits; Transmembrane;  
 KW Receptor; EGF-like domain; SH3-binding; Signal.  
 FT SIGNAL 1 25  
 FT CHAIN 26 4660  
 FT DOMAIN 26 4425  
 FT TRANSMEM 4426 4446  
 FT DOMAIN 4447 4660  
 FT DOMAIN 26 64  
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 FT DOMAIN 23076 23116  
 FT DOMAIN 23116 23156  
 FT DOMAIN 23156 23196  
 FT DOMAIN 23196 23236  
 FT DOMAIN 23236 23276  
 FT DOMAIN 23276 23316  
 FT DOMAIN 23316 23356  
 FT DOMAIN 23356 23396  
 FT DOMAIN 23396 23436  
 FT DOMAIN 23436 23476  
 FT DOMAIN 23476 23516  
 FT DOMAIN 23516 23556  
 FT DOMAIN 23556 23596  
 FT DOMAIN 23596 23636  
 FT DOMAIN 23636 23676  
 FT DOMAIN 23676 23716  
 FT DOMAIN 23716 23756  
 FT DOMAIN 23756 23796  
 FT DOMAIN 23796 23836  
 FT DOMAIN 23836 23876  
 FT DOMAIN 23876 23916  
 FT DOMAIN 23916 23956  
 FT DOMAIN 23956 23996  
 FT DOMAIN 23996 24036  
 FT DOMAIN 24036



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CC EMBL; J02890; AAA30356.1; -  
 DR EMBL; J05160; AAA30490.1; ALT\_INIT.  
 DR HSSP; P14925; 1PHM.  
 DR InterPro; IPR000323; Cu2\_monooxygenase.  
 DR InterPro; IPR000945; DB\_monooxygenase.  
 DR InterPro; IPR005018; DOMON.  
 DR InterPro; IPR008977; PHM\_PNGase\_F.  
 DR Pfam; PF03712; Cu2\_monoox\_C; 1.  
 DR Pfam; PF01082; Cu2\_monooxygen; 1.  
 DR Pfam; PF03351; DOMON; 1.  
 DR PRINTS; PR00767; DBMONOXGNASE.  
 DR SMART; SM00664; DOH; 1.  
 DR PROSITE; PS00084; CU2\_MONOOXYGENASE\_1; 1.  
 DR PROSITE; PS00085; CU2\_MONOOXYGENASE\_2; 1.  
 DR PROSITE; PS00836; DOMON; 1.  
 KW Catecholamine biosynthesis; Oxidoreductase; Monooxygenase; Copper;  
 FT Vitamin C; PQ; Glycoprotein; Membrane; Signal.  
 FT SIGNAL 1 32  
 FT CHAIN 33 610 DOPAMINE BETA-MONOOXYGENASE.  
 FT DOMAIN 50 166  
 FT ACT\_SITE 223 223 POTENTIAL.  
 FT ACT\_SITE 405 405 POTENTIAL.  
 FT METAL 405 405 COPPER (POTENTIAL).  
 FT DISULFID 147 589  
 FT DISULFID 225 276  
 FT DISULFID 262 288  
 FT DISULFID 383 496  
 FT DISULFID 387 558  
 FT DISULFID 459 481  
 FT DISULFID 521 521  
 FT DISULFID 523 523  
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 559 559 N-LINKED (GLCNAC. . .).  
 FT CONFLICT 35 35 P -> T (IN REF. 4).  
 FT CONFLICT 48 48 P -> T (IN REF. 4).  
 FT CONFLICT 55 57 SWN -> RYV (IN REF. 3).  
 FT CONFLICT 74 74 L -> F (IN REF. 3).  
 FT CONFLICT 205 205 R -> C (IN REF. 2).  
 FT CONFLICT 267 269 RDH -> ETI (IN REF. 2).  
 FT CONFLICT 560 560 R -> C (IN REF. 3).  
 FT CONFLICT 588 588 Q -> H (IN REF. 2).  
 SQ SEQUENCE 610 AA; 68143 MW; 1639DB670F94DE71 CRC64;

Query Match 3.9%; Score 8; DB 1; Length 610;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 144 AVAVFLVI 151  
 DB 18 AVAVFLVI 25

RESULT 5  
 ID\_NPHN\_HUMAN STANDARD; PRT; 1241 AA.  
 AC O60500;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Nephtrin precursor (Renal glomerulus-specific cell adhesion receptor).  
 GN NPHS1 OR NPHN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=98325371; PubMed=9660941;  
 RA Kestilae M., Lenkkeri U., Maennikoe M., Lamerdin J., McCready P.,  
 RA Putaala H., Ruotalainen V., Morita T., Nissinen M., Hervä R.,  
 RA Kashtan C.R., Peltonen L., Holmberg C., Olsen A., Tryggvason K.;  
 RT "Positionally cloned gene for a novel glomerular protein -- nephrin --  
 RT is mutated in congenital nephrotic syndrome.";  
 RL Mol. Cell 1:575-582(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX Grunkemeyer J.A., Kumar N., Kalluri R.;  
 RT "Human nephrin (NPHS1) cDNA sequence.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 1032-1134 FROM N.A. (ISOFORM 2), AND SUBCELLULAR LOCATION.  
 RX MEDLINE=20019662; PubMed=10550324;  
 RA Holthofer H., Ahola H., Solin M.-L., Wang S.-X., Palmen T.,  
 RA Luimula P., Miettinen A., Kerjaschki D.;  
 RT "Nephtrin localizes at the podocyte filtration slit area and is  
 RT characteristically spliced in the human kidney.";  
 RL Am. J. Pathol. 155:1681-1687(1999).  
 RN [4]  
 RP SUBCELLULAR LOCATION.  
 RX MEDLINE=99324171; PubMed=10393930;  
 RA Ruotalainen V., Ljungberg P., Wartiovaara J., Lenkkeri U.,  
 RA Kestilae M., Jalanko H., Holmberg C., Tryggvason K.;  
 RT "Nephtrin is specifically located at the slit diaphragm of glomerular  
 RT podocytes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:7962-7967(1999).  
 RN [5]  
 RP INTERACTION WITH NPHS2.  
 RX MEDLINE=21551283; PubMed=11562357;  
 RA Huber T.B., Kottgen M., Schilling B., Walz G., Benzing T.;  
 RT "Interaction with podocin facilitates nephrin signaling.";  
 RL J. Biol. Chem. 276:41543-41546(2001).  
 RN [6]  
 RP VARIANTS LYS-117 AND SER-1077, AND VARIANTS CNP SER-64; ASN-171;  
 RP THR-172 DEL; ASN-173; 205-THR-ARG-207 DELINS ILE; CYS-270;  
 RP PRO-350; ARG-366; CYS-367; SER-368; VAL-376; GLN-408; TYR-465;  
 RP PHE-528; GLN-610; PHE-623; CYS-724; CYS-743; TRP-802; PRO-802;  
 RP ASP-806; CYS-831 AND CYS-1140.  
 RX MEDLINE=99115081; PubMed=9915943;  
 RA Lenkkeri U., Maennikoe M., McCready P., Lamerdin J., Gribouval O.,  
 RA Naudet P.M., Aignac C.K., Kashtan C.E., Homberg C., Olsen A.,  
 RA Kestilae M., Tryggvason K.;  
 RT "Structure of the gene for congenital nephrotic syndrome of the  
 RT Finnish type (NPHS1) and characterization of mutations.";  
 RL Am. J. Hum. Genet. 64:51-61(1999).  
 RN [7]  
 RP VARIANTS CNP LYS-447 AND VAL-819.  
 RX MEDLINE=20117947; PubMed=10652016;  
 RA Aya K., Tanaka H., Seino Y.;  
 RT "Novel mutation in the nephrin gene of a Japanese patient with  
 RT congenital nephrotic syndrome of the Finnish type.";  
 RL Kidney Int. 57:401-404(2000).  
 CC -!- FUNCTION: Seems to play a role in the development or function of  
 CC the kidney glomerular filtration barrier. May anchor the podocyte  
 CC slit diaphragm to the actin cytoskeleton.  
 CC -!- SUBUNIT: Interacts with podocin/NPHS2. Interacts with CD2AP C-  
 CC terminal domain (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC Predominantly located at podocyte slit diaphragm between podocyte  
 CC foot processes. Also associated with podocyte apical plasma  
 CC membrane.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=O60500-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Alpha;  
 CC IsoId=O60500-2; Sequence=VSP\_002598;  
 CC -!- TISSUE SPECIFICITY: Specifically expressed in podocytes of kidney  
 CC glomeruli.  
 CC -!- DEVELOPMENTAL STAGE: In 23-week-old embryo found in epithelial



RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
 RA Peterson S., Reich C.I., McNeill L.K., Badger J.H., Glodok A., Zhou L.,  
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uterback T.,  
 RA Cotton M.D., Spraygs T., Artlich P., Kaine B.P., Sykes S.M.,  
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
 RA Venter J.C.;  
 RA "The complete genome sequence of the hyperthermophilic, sulphate-  
 RT reducing archaeon *Archaeoglobus fulgidus*.";  
 RL Nature 390:364-370(1997).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
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 CC -----  
 DR EMBL; AB001064; AAB90659.1; -;  
 DR PIR; A69423; A69323.  
 DR TIGR; AF0585; -;  
 DR KW Hypothetical protein; Transmembrane; Complete proteome.  
 FT TRANSMEM 5 27 POTENTIAL.  
 FT TRANSMEM 40 62 POTENTIAL.  
 FT TRANSMEM 67 89 POTENTIAL.  
 SQ SEQUENCE 90 AA; 10081 MW; CSD18CF7C03B4226 CRC64;  
 Query Match 3.4%; Score 7; DB 1; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 3.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 154 VVVVAIL 160  
 Db 69 VVVVAIL 75  
 RESULT 7  
 XAL7 HUMAN  
 ID XAL7 HUMAN STANDARD; PRT; 114 AA.  
 AC Q3113; Q96E11;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE 17 kDa membrane associated protein (DD96 protein).  
 GN MAP17.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RC MEDLINE=99034932; PubMed=9815914;  
 RA Koehler O., Cheres P., Brown L.F., Lee S.W.;  
 RT "Identification of a novel gene, selectively up-regulated in human  
 RL Clin. Cancer Res. 1:1209-1215(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Grafham D.;  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RC MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergran E.J., Lu X., Gibbs R.A., Sanchez A.,  
 RA Fahy J., Heiton E., Kettman M., Madan A., Rodriguez S., Bouffard G.G.,  
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield A.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC [4]  
 CC CHARACTERIZATION.  
 CC MEDLINE=96312852; PubMed=8701988;  
 CC Koehler O., Cheres P., Lee S.W.;  
 RT "Identification and partial characterization of a novel membrane-  
 RT associated protein (MAP17) up-regulated in human carcinomas and  
 RT modulating cell replication and tumor growth.";  
 RL Am. J. Pathol. 149:493-500(1996).  
 CC -1- FUNCTION: May play an important role in tumor biology.  
 CC -1- SUBCELLULAR LOCATION: Membrane-associated.  
 CC -1- TISSUE SPECIFICITY: Expressed at significant levels only in a  
 CC single epithelial cell population, the proximal tubular epithelial  
 CC cells of the kidney. Diffusely expressed in various carcinomas  
 CC originating from kidney, colon, lung and breast.  
 CC -----  
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 CC -----  
 DR EMBL; U21049; AAA92690.1; -;  
 DR EMBL; AL135960; CAB72104.1; -;  
 DR EMBL; BC012303; AAH12303.1; -;  
 DR MIM; 607178; -;  
 KW Transmembrane.  
 FT TRANSMEM 33 50 POTENTIAL.  
 FT CONFLICT 13 13 T -> M (IN REF. 3).  
 FT CONFLICT 51 51 N -> K (IN REF. 3).  
 SQ SEQUENCE 114 AA; 12227 MW; 7DBE64C3AF78CB18 CRC64;  
 Query Match 3.4%; Score 7; DB 1; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 4.4;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 144 AVAVPLV 150  
 Db 36 AVAVPLV 42  
 RESULT 8  
 RZPR ECOLI  
 ID RZPR ECOLI STANDARD; PRT; 147 AA.  
 AC P77551;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Putative R2 endopeptidase from lambdoid prophage Rac (EC 3.4.-.-)  
 DE (Fragment).  
 GN RZPR OR B1362.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=X12 / MG1655;

```

RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nasimoto H., Nishio Y., Oshima T., Saito N.,
RA Sampi G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takenoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-Kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
CC -|- FUNCTION: Necessary for host cell lysis. It is believed to code
CC for an endopeptidase that cleaves the amino-carboxyl cross-link
CC between the diaminopimelic acid and D-alanine residues in the
CC mature component of the bacterial cell wall (By similarity).
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY U8. STRONG, TO LAMBDOID
CC PHAGES ENDOPEPTIDASES.
CC -----
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CC -----
CC EMBL; AE000233; AAC74444.1; ALT INIT.
CC EMBL; D90774; BAA14959.1; ALT_INIT.
CC EcoGene; EG13366; rzpr.
CC InterPro; IPR004929; Phage_lysis.
CC Pfam; PF03245; Phage_lysis; 1.
CC Hypothetical protein; Hydrolase; Protease; Bacteriolytic enzyme;
CC Complete proteome.
CC NON TER 1
CC SEQUENCE 147 AA; 16486 MW; 2F4B85F6663A7692 CRC64;

Query Match 3.4%; Score 7; DB 1; Length 147;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 LVICIV 155
DB 4 LVICIV 10
|||||

RESULT 9
APL LACLC
ID APL LACLC STANDARD; PRT; 242 AA.
AC Q48530;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alkaline phosphatase like protein.
GN APL.
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=Mg1363;
RA Venema K., Haandrikman A., Leenhouts K., Kok J., Venema G.;
RT "Cloning and sequencing of a gene (apl) from Lactococcus lactis that
RT can complement a phoA mutation in Escherichia coli.";
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.

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CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -|- SIMILARITY: Belongs to the dedA family.
CC -----
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CC -----
CC EMBL; Z29065; CAA82306.1; -.
CC PIR; S39339; S39339.
CC InterPro; IPR000252; DedA.
CC Pfam; PF00597; DedA; 1.
CC Transmembrane.
CC TRANSMEM 48 68 POTENTIAL.
CC TRANSMEM 141 161 POTENTIAL.
CC TRANSMEM 177 197 POTENTIAL.
CC SEQUENCE 242 AA; 27134 MW; 650A8B314C44BA55 CRC64;

Query Match 3.4%; Score 7; DB 1; Length 242;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 VVVAIIG 161
DB 180 VVVAIIG 186
|||||

RESULT 10
CAHC HUMAN
ID CAHC HUMAN STANDARD; PRT; 354 AA.
AC Q43570; Q9BWC2;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Carbonic anhydrase XII precursor (EC 4.2.1.1) (Carbonate dehydratase
DE XII) (CA-XII) (Tumor antigen HOM-RCC-3.1.3).
GN CA12.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC TISSUE=Renal cell carcinoma;
RX MEDLINE=98301622; PubMed=9636197;
RA Tuercio O., Sahin U., Vollmar E., Siemer S., Goettert E., Seitz G.,
RA Parkkila A.-K., Shah G.N., Grubb J.H., Pfeundschtuh M., Sly W.S.;
RT "Human carbonic anhydrase XII: cDNA cloning, expression, and
RT chromosomal localization of a carbonic anhydrase gene that is
RT overexpressed in some renal cell cancers.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:7608-7613(1998).
RN [2];
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=lung;
RX MEDLINE=9845416; PubMed=9770531;
RA Ivanov S.V., Kuzmin I., Wei M.-H., Pack S., Geil L., Johnson B.E.,
RA Stanbridge E.J., Lerman M.I.;
RT "Down-regulation of transmembrane carbonic anhydrases in renal cell
RT carcinoma cell lines by wild-type von Hippel-Lindau transgenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:12596-12601(1998).
RN [3];
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Eye, and Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RA "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 30-292.  
RX MEDLINE=21396545; PubMed=11493685;  
RA Whittington D.A., Waheed A., Ulmasov B., Shah G.N., Grubb J.H.,  
RA Sly W.S., Christianson D.W.;  
RT "Crystal structure of the dimeric extracellular domain of human  
RT carbonic anhydrase XII, a bitopic membrane protein overexpressed in  
RT certain cancer tumor cells.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9545-9550 (2001).  
CC -!- FUNCTION: Reversible hydration of carbon dioxide.  
CC -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.  
CC -!- COPACTOR: Zinc (by similarity).  
CC -!- ENZYME REGULATION: Inhibited by acetazolamide.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=O43570-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=O43570-2; Sequence=VSP\_000772;  
CC Note=No experimental confirmation available;  
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COLON, KIDNEY, PROSTATE,  
CC INTESTINE AND ACTIVATED LYMPHOCYTES. EXPRESSED AT MUCH HIGHER  
CC LEVELS IN THE RENAL CELL CANCERS THAN IN SURROUNDING NORMAL KIDNEY  
CC TISSUE. MODERATELY EXPRESSED IN PANCREAS, OVARY, AND TESTIS.  
CC -!- SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase  
CC family.  
CC  
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CC -----  
DR EMBL; AF051892; AAC39789.1; -;  
DR EMBL; AF037335; AAC63952.1; -;  
DR EMBL; BC000278; AAH00278.1; -;  
DR EMBL; BC011631; AAH11631.1; -;  
DR EMBL; BC023981; AAH23981.1; -;  
DR PDB; 1JD0; 17-AUG-01.  
DR PDB; 1JCZ; 17-AUG-01.  
DR Genes; HGNC:1371; CA12.  
DR MIM; 603263; -;  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0004089; F:carbonate dehydratase activity; TAS.  
DR GO; GO:0008270; F:zinc ion binding; TAS.  
DR InterPro; IPR001148; Ruk Coanhd.  
DR Pfam; PF00194; carb anhydrase; 1.  
DR ProDom; PD000865; Euk Coanhd; 1.  
DR PROSITE; PS00162; EUK\_CO2\_ANHYDRASE; 1.  
DR Lyase; Zinc; Transmembrane; Signal; Alternative splicing;  
KW 3D-structure. 1 24  
FT SIGNAL 25 354 POTENTIAL.  
FT CHAIN 25 354 CARBONIC ANHYDRASE XII.  
FT DOMAIN 25 301 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 302 322 POTENTIAL.  
FT DOMAIN 323 354 CYTOPLASMIC (POTENTIAL).

FT METAL 119 119 ZINC (CATALYTIC).  
FT METAL 121 121 ZINC (CATALYTIC).  
FT METAL 145 145 ZINC (CATALYTIC).  
FT DISULFID 50 230  
FT CARBOHYD 80 28 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPLIC 292 302 Missing (in isoform 2).  
/FTId=VSP\_000772.  
FT TURN 37 38  
FT HELIX 40 42  
FT HELIX 43 46  
FT HELIX 48 51  
FT STRAND 59 60  
FT HELIX 62 64  
FT STRAND 65 67  
FT TURN 69 70  
FT STRAND 75 77  
FT STRAND 80 80  
FT TURN 83 84  
FT STRAND 86 91  
FT STRAND 96 99  
FT TURN 102 103  
FT STRAND 105 107  
FT STRAND 111 122  
FT STRAND 124 124  
FT TURN 125 126  
FT STRAND 127 127  
FT STRAND 134 135  
FT TURN 136 137  
FT STRAND 138 138  
FT STRAND 142 150  
FT TURN 151 153  
FT HELIX 157 160  
FT TURN 161 162  
FT TURN 164 165  
FT STRAND 167 176  
FT HELIX 181 187  
FT TURN 188 189  
FT HELIX 190 193  
FT TURN 196 197  
FT STRAND 199 203  
FT STRAND 206 206  
FT HELIX 207 210  
FT TURN 215 216  
FT STRAND 218 223  
FT TURN 228 229  
FT STRAND 234 239  
FT STRAND 243 245  
FT HELIX 247 255  
FT STRAND 258 258  
FT TURN 262 263  
FT STRAND 269 269  
FT STRAND 285 287  
SQ SEQUENCE 354 AA; 39451 MW; 9016216BF2CA6C0C CRC64;  
Query Match 3.4%; Score 7; DB 1; Length 354;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 151 ICIVVVV 157  
Db 316 ICIVVVV 322  
|||||  
RESULT 11  
QIN\_AVIS3  
ID QIN\_AVIS3 STANDARD; PRT; 387 AA.  
AC P56260;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Transforming protein Qin (Oncogene Qin).

GN V-QIN.  
OS Avian sarcoma virus (strain 31) (ASV31).  
OC Viruses; Retroviral viruses; Retroviridae; Avian type C retroviruses.  
OX NCBI\_TaxID=35270;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93281605; PubMed=8099441;  
RA Li J., Vogt P.K.;  
RT "The retroviral oncogene qin belongs to the transcription factor  
RT family that includes the homeotic gene fork head.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:4490-4494(1993).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-QIN  
CC POLYPEPTIDE.  
CC -!- SIMILARITY: Contains 1 fork-head domain.  
CC  
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CC  
CC EMBL; L10719; -; NOT\_ANNOTATED\_CDS.  
DR HSP; Q63245; 2HFH.  
DR TRANSFAC; T01832; -.  
DR InterPro; IPR001766; TF\_Fork\_head.  
DR Pfam; PF00250; Fork\_head; 1.  
DR PRINTS; PR00053; FORKHEAD.  
DR ProDom; PD000425; TF\_Fork\_head; 1.  
DR SMART; SM00339; FH; 1.  
DR PROSITE; PS00657; FORK\_HEAD\_1; 1.  
DR PROSITE; PS00658; FORK\_HEAD\_2; 1.  
DR PROSITE; PS50039; FORK\_HEAD\_3; 1.  
DR DNA-binding; Nuclear protein; Oncogene.  
KW DOMAIN 42 54  
FT DOMAIN 55 58 POLY-HIS.  
FT DOMAIN 64 67 POLY-ALA.  
FT DOMAIN 101 106 POLY-ALA.  
FT DNA\_BIND 142 233 FORK-HEAD.  
FT SEQUENCE 387 AA; 42283 MW; FEA902F50FFB42F9 CRC64;  
SQ

Query Match 3.4%; Score 7; DB 1; Length 387;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 175 HHHHPP 181  
|||  
DB 51 HHHHPP 57

RESULT 12  
BRNQ\_HAEIN  
ID BRNQ\_HAEIN STANDARD; PRT; 436 AA.  
AC P71345;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Branched-chain amino acid transport system carrier protein (Branched-  
DE chain amino acid uptake carrier).  
GN BRNQ OR H10226;  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Haemophilus.  
OX NCBI\_TaxID=727;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=Rd / KW20 / ATCC 51907;  
RX MEDLINE=9530630; PubMed=7542800;  
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.P.,  
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
RA Weidman J.P., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
RA Fise L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,  
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
RA Venter J.C.;  
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae  
RT Rd.";  
RL Science 269:496-512(1995).  
CC -!- FUNCTION: Component of the transport system for branched-chain  
CC amino acids (leucine, isoleucine and valine) which is coupled to a  
CC proton motive force (By similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.  
CC -!- SIMILARITY: BELONGS TO THE BRAC/BRAB/BRNQ FAMILY OF TRANSPORTERS.  
CC  
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CC  
CC EMBL; U32709; AAC21896.1; -.  
DR PIR; D64056; D64056.  
DR TIGR; H10226; -.  
DR InterPro; IPR004685; Livcs.  
DR Pfam; PF05525; Branch\_AA\_trans; 1.  
DR TIGRFAMs; TIGR00796; Livcs; 1.  
KW Amino-acid transport; Transport; Transmembrane; Inner membrane;  
KW Complete proteome.  
FT TRANSMEM 7 27 POTENTIAL.  
FT TRANSMEM 43 63  
FT TRANSMEM 76 96 POTENTIAL.  
FT TRANSMEM 122 142 POTENTIAL.  
FT TRANSMEM 148 168 POTENTIAL.  
FT TRANSMEM 185 205 POTENTIAL.  
FT TRANSMEM 228 248 POTENTIAL.  
FT TRANSMEM 277 297 POTENTIAL.  
FT TRANSMEM 314 334 POTENTIAL.  
FT TRANSMEM 339 359 POTENTIAL.  
FT TRANSMEM 411 431 POTENTIAL.  
FT SEQUENCE 436 AA; 47039 MW; FA37EDF6C2193DF CRC64;  
SQ

Query Match 3.4%; Score 7; DB 1; Length 436;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 155 VVVAIIG 161  
|||  
DB 58 VVVAIIG 64

RESULT 13  
FXGB\_CHICK  
ID FXGB\_CHICK STANDARD; PRT; 451 AA.  
AC Q90964;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Forkhead box protein, G1B (Forkhead-related protein FKHL1)  
DE (transcription factor BF-1) (Brain factor 1) (BF1) (CBF-1) (Proto-  
DE oncogene C-QIN) (N-62-5) (CBQ 3-1).  
GN FOXG1B OR FKHL1 OR QIN.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95132616; PubMed=7831308;  
RA Chang H.W., Li J., Kretzschmar D., Vogt P.K.;



RT "Avian cellular homolog of the qin oncogene.";   
 RL Proc. Natl. Acad. Sci. U.S.A. 92:447-451(1995).   
 RN [2]   
 RP SEQUENCE FROM N.A.   
 RC STRAIN=White leghorn; TISSUE=Retina;   
 RA MEDLINE=96338226; PubMed=8757134;   
 RX Yuasa J., Hirano S., Yanagata M., Noda M.;   
 RT "Visual projection map specified by topographic expression of   
 RT transcription factors in the retina.";   
 RL Nature 382:632-635(1996).   
 CC -!- FUNCTION: May determine the nasotemporal axis of the retina, and   
 CC consequently specify the topographical projection of the retinal   
 CC ganglion-cell axons to the tectum by controlling expression of   
 CC their target genes.   
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).   
 CC -!- TISSUE SPECIFICITY: Retina and brain.   
 CC -!- DEVELOPMENTAL STAGE: Can be detected in regions including   
 CC primordial retina and neuroepithelium by embryonic day 2 (E2). At   
 CC E3, expressed in the nasal retina and pigment epithelium as well   
 CC as in the telencephalon, and at E7 is expressed in retinal   
 CC ganglion cells. Levels begin to decline from E4 and almost   
 CC disappear by E10.   
 CC -!- SIMILARITY: Contains 1 fork-head domain.   
 CC -----   
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 CC -----   
 DR EMBL; L36814; AAA66954.1; -   
 DR EMBL; U47275; AB308466.1; -   
 DR PIR; A55909; A55909.   
 DR HSSP; Q63245; 2HFH.   
 DR TRANSFAC; T01833; -   
 DR InterPro; IPR001766; TF\_Fork\_head.   
 DR Pfam; PF00250; Fork\_head; 1.   
 DR PRINTS; PR00053; FORKHEAD.   
 DR ProDom; PD000425; TF\_Fork\_head; 1.   
 DR SMART; SM00339; FH; 1.   
 DR PROSITE; PS00657; FORK\_HEAD\_1; 1.   
 DR PROSITE; PS00658; FORK\_HEAD\_2; 1.   
 DR PROSITE; PS00039; FORK\_HEAD\_3; 1.   
 DR Transcription regulation; DNA-binding; Nuclear protein;   
 KW Developmental protein; Proto-oncogene.   
 FT DOMAIN 45 54 POLY-HIS.   
 FT DOMAIN 55 58   
 FT DOMAIN 64 67 POLY-PRO.   
 FT DOMAIN 103 106 POLY-ALA.   
 FT DOMAIN 142 233 POLY-ALA.   
 FT DNA BIND 142 233 FORK-HEAD.   
 SQ SEQUENCE 451 AA; 48856 MW; E95B407D2321B50 CRC64;   
 Query Match 3.4%; Score 7; DB 1; Length 451;   
 Best Local Similarity 100.0%; Pred. No. 15;   
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;   
 QY 175 HHHHPPP 181   
 Db 51 HHHHPPP 57   
 RESULT 14   
 ID FXGA\_HUMAN STANDARD; PRT; 469 AA.   
 AC P5316;   
 DT 01-OCT-1996 (Rel. 34, Created)   
 DT 01-OCT-1998 (Rel. 34, Last sequence update)   
 DT 16-OCT-2001 (Rel. 40, Last annotation update)   
 DE Forkhead box protein GLA (Forkhead-related protein FXHL2)   
 DE {Transcription factor BF-2} (Brain factor 2) (BF2) (HFK2).   
 GN FOXGLA OR FXHL2.

OS Homo sapiens (Human).   
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.   
 OC NCBI\_TaxID=9606;   
 RN [1]   
 RP SEQUENCE FROM N.A.   
 RC TISSUE=Brain;   
 RX MEDLINE=95048332; PubMed=7959731;   
 RA Murphy D.B., Wiese S., Burfeind P., Schmundt D., Mattei M.-G.,   
 RA Schulz-Schaeffer W., Thies U.;   
 RT "Human brain factor 1, a new member of the fork head gene family.";   
 RL Genomics 21:551-557(1994).   
 CC [2]   
 CC SEQUENCE FROM N.A.   
 CC MEDLINE=95322450; PubMed=7599184;   
 CC Wiese S., Murphy D.B., Schlung A., Burfeind P., Schmundt D.,   
 CC Schunle V., Mattei M.-G., Thies U.;   
 CC "The genes for human brain factor 1 and 2, members of the fork head   
 CC gene family, are clustered on chromosome 14q.";   
 CC Biochim. Biophys. Acta 1262:105-112(1995).   
 CC -!- FUNCTION: Plays an important role in the establishment of the   
 CC regional subdivision of the developing brain and in the   
 CC development of the telencephalon. Sequence-specific DNA-binding   
 CC protein with a distinct binding specificity (by similarity).   
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).   
 CC -!- SIMILARITY: Contains 1 fork-head domain.   
 CC -----   
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 CC -----   
 DR EMBL; X78202; CAA55038.1; -   
 DR EMBL; X74143; CAA52240.1; -   
 DR PIR; I37451; I37451.   
 DR HSSP; Q63245; 2HFH.   
 DR TRANSFAC; T02292; -   
 DR Genew; HGNC.3811; FOXGLA.   
 DR MIM; 600779; -   
 DR GO; GO:0003677; F:DNA binding; TAS.   
 DR GO; GO:0007420; P:brain development; TAS.   
 DR InterPro; IPR001766; TF\_Fork\_head.   
 DR Pfam; PF00250; Fork\_head; 1.   
 DR PRINTS; PR00053; FORKHEAD.   
 DR ProDom; PD000425; TF\_Fork\_head; 1.   
 DR SMART; SM00339; FH; 1.   
 DR PROSITE; PS00657; FORK\_HEAD\_1; 1.   
 DR PROSITE; PS00658; FORK\_HEAD\_2; 1.   
 DR PROSITE; PS00039; FORK\_HEAD\_3; 1.   
 DR Transcription regulation; DNA-binding; Nuclear protein;   
 KW Developmental protein.   
 FT DOMAIN 33 56 HIS-RICH.   
 FT DOMAIN 57 79 PRO-RICH.   
 FT DOMAIN 70 73 POLY-GLN.   
 FT DOMAIN 83 88 POLY-ARG.   
 FT DNA BIND 161 252 FORK-HEAD.   
 SQ SEQUENCE 469 AA; 50539 MW; 943BBDB90008EDC CRC64;   
 Query Match 3.4%; Score 7; DB 1; Length 469;   
 Best Local Similarity 100.0%; Pred. No. 16;   
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;   
 QY 175 HHHHPPP 181   
 Db 54 HHHHPPP 60   
 RESULT 15   
 ID FXGB\_HUMAN STANDARD; PRT; 477 AA.   
 GN FOXGLA\_HUMAN

```
AC P55315;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Forkhead box protein G1B (Forkhead-related protein FKHL1)
GN (Transcription factor BF-1) (Brain factor 1) (BFL) (FKL1)
GN FOXG1B OR FKHL1
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95049332; PubMed=7959731;
RA Murphy D.B., Wiese S., Burfeind P., Schmundt D., Mattei M.-G.,
RA Schulz-Schaeffer W., Thies U.;
RT "Human brain factor 1, a new member of the fork head gene family.";
RL Genomics 21:551-557(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95322450; PubMed=7599184;
RA Wiese S., Murphy D.B., Schlung A., Burfeind P., Schmundt D.,
RA Schmulle V., Mattei M.-G., Thies U.;
RT "The genes for human brain factor 1 and 2, members of the fork head
RT gene family, are clustered on chromosome 14q.";
RL Biochim. Biophys. Acta 1262:105-112(1995).
CC -!- FUNCTION: Plays an important role in the establishment of the
CC regional subdivision of the developing brain and in the
CC development of the telencephalon. Sequence-specific DNA-binding
CC protein with a distinct binding specificity (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Contains 1 fork-head domain.
CC -----
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CC -----
DR EMBL; X74142; CAA52239.1; -
DR HSSP; Q63245; 2HFH.
DR TRANSFAC; T02350; -
DR Genew; HGNC:3812; FOXG1B.
DR MIM; 164874; -
DR GO; GO:0003677; F-DNA binding; TAS.
DR GO; GO:0007420; F-brain development; TAS.
DR InterPro; IPR001766; TF_Fork_head.
DR Pfam; PF0250; Fork_head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00657; FORK_HEAD_1; 1.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS00039; FORK_HEAD_3; 1.
KW Transcription regulation; DNA-binding; Nuclear protein;
KW Developmental protein.
FT DOMAIN 33 57 HIS-RICH.
FT DOMAIN 58 80 PRO-RICH.
FT DOMAIN 72 75 POLY-GLN.
FT DOMAIN 99 102 POLY-LEU.
FT DNA_BIND 168 259 FORK-HEAD.
SQ SEQUENCE 477 AA; 51340 MW; 71CFD0BD069CFAD5 CRC64;

Query Match 3.4%; Score 7; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 175 HHHPPP 181

|||||

Db 54 HHHPPP 60

Search completed: April 22, 2004, 10:24:02  
Job time : 19 secs

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OM protein - protein search, using sw model

Run on: April 22, 2004, 10:15:30 ; Search time 26 Seconds  
(without alignments)  
762.133 Million cell updates/sec

Title: US-09-935-390A-23  
Perfect score: 206  
Sequence: 1 MERRHPVCSGTCQTPQRCs.....TVSTTDETHLVNHTTREL 206

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues  
Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 78.\*  
1: Piri.\*  
2: Piri.\*  
3: Piri.\*  
4: Piri.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	5.3	972	2 A30363	glycoprotein GP330
2	11	5.3	4660	2 T42737	gp330 protein precursor - rat
3	8	3.9	610	2 A33650	dopamine beta-mono
4	8	3.9	759	2 D89946	protein-export mem
5	8	3.9	1241	2 T37190	nephritin - human
6	8	3.9	1743	2 T26859	hypothetical prote
7	7	3.4	90	2 A69323	hypothetical prote
8	7	3.4	116	2 E48338	hypothetical prote
9	7	3.4	135	2 G97172	hypothetical prote
10	7	3.4	152	2 S49230	glycine cleavage s
11	7	3.4	159	2 T38729	hypothetical prote
12	7	3.4	161	2 S60198	glycine cleavage s
13	7	3.4	173	2 A72620	probable NADH dehy
14	7	3.4	202	2 D87019	cytochrome C oxida
15	7	3.4	217	2 A13429	transposase BME114
16	7	3.4	221	2 S20964	ribosomal protein
17	7	3.4	222	2 T03540	cobalamin biosynth
18	7	3.4	222	2 H96711	hypothetical prote
19	7	3.4	242	2 S39339	alkaline phosphata
20	7	3.4	256	2 H36857	B26R protein - var
21	7	3.4	281	2 T20743	hypothetical prote
22	7	3.4	283	2 B69713	required for compl
23	7	3.4	288	2 T17737	proline-rich prote
24	7	3.4	317	2 AC0464	cell division prot
25	7	3.4	346	2 E89036	hypothetical prote
26	7	3.4	368	2 T36414	probable iron-side
27	7	3.4	387	2 A47446	ENF-3/fork head fa
28	7	3.4	388	2 T18937	hypothetical prote
29	7	3.4	394	2 T20633	hypothetical prote

30	7	3.4	405	2 T21188	hypothetical prote
31	7	3.4	408	2 B81417	hypothetical prote
32	7	3.4	436	2 D64056	branched-chain ami
33	7	3.4	451	2 A55909	transforming prote
34	7	3.4	460	1 S51516	serine-type carbox
35	7	3.4	469	2 I37451	HBP-G2 (HFK-2) pro
36	7	3.4	476	2 A54743	transcription fact
37	7	3.4	480	2 JH0672	brain factor 1 pro
38	7	3.4	481	2 JH0377	p70 S6 kinase (EC
39	7	3.4	512	2 E96024	conserved hypothet
40	7	3.4	525	1 A41687	ribosomal protein
41	7	3.4	525	1 TVR1K6	probable ribosomal
42	7	3.4	525	1 S12906	ucharakterized pro
43	7	3.4	527	2 C97170	chacterized pro
44	7	3.4	537	2 AB2766	sulfate permease [
45	7	3.4	537	2 F97546	hypothetical prote

ALIGNMENTS

RESULT 1

A30363  
Glycoprotein GP330, renal - rat (fragments)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 18-Aug-2000  
C:Accession: A30363  
R:Raychowdhury, R.; Niles, J.L.; McCluskey, R.T.; Smith, J.A.  
Science 244, 1163-1165, 1989  
A:Title: Autoimmune target in Heymann nephritis is a glycoprotein with homology to the  
A:Reference number: A30363; MUID:89266937; PMID:2786251  
A:Accession: A30363  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-972 <RAY>  
C:Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding  
C:Keywords: glycoprotein  
F:24-53/Domain: EGF homology <EGF>  
F:64-98/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
F:105-140/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
F:149-183/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
F:189-223/Domain: LDL receptor ligand-binding repeat homology <LDL4>  
F:227-262/Domain: LDL receptor ligand-binding repeat homology <LDL5>  
F:270-306/Domain: LDL receptor ligand-binding repeat homology <LDL6>  
F:311-345/Domain: LDL receptor ligand-binding repeat homology <LDL7>  
F:352-388/Domain: LDL receptor ligand-binding repeat homology <LDL8>  
F:396-430/Domain: LDL receptor ligand-binding repeat homology <LDL9>  
F:435-469/Domain: LDL receptor ligand-binding repeat homology <LDL10>  
F:479-515/Domain: LDL receptor ligand-binding repeat homology <LDL11>  
F:520-557/Domain: LDL receptor ligand-binding repeat homology <LDL12>  
F:565-599/Domain: LDL receptor ligand-binding repeat homology <LDL13>  
F:705-747/Domain: LDL receptor YWTD-containing repeat homology <YWI>  
F:748-791/Domain: LDL receptor YWTD-containing repeat homology <YW2>  
F:793-832/Domain: LDL receptor YWTD-containing repeat homology <YW3>

Query Match 5.3%; Score 11; DB 2; Length 972;

Best Local Similarity 100.0%; Pred. No. 0.0044;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SCTCQPTQPRC 19

DB 186 SGTCTQPTQPRC 196

RESULT 2

T42737  
gp330 protein precursor - rat  
N:Alternate names: megalin  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 04-Mar-2000  
C:Accession: T42737  
R:Saito, A.; Pietromonaco, S.; Loo, A.K.C.; Farquhar, M.G.  
Proc. Natl. Acad. Sci. U.S.A. 91, 9725-9729, 1994

A:Title: Complete cloning and sequencing of rat gp330/megalin, a distinctive member of the A:Reference number: A58173; MUID:95024033; PMID:7937880  
A:Accession: T42737  
A>Status: Preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-4660 <SAI>  
A:Cross-references: EMBL:U34049; NID:G561852; PID:G561853; PIDN:AAA51369.1  
A:Experimental source: strain Sprague-Dawley; kidney  
C:Superfamily: alpha-2-macroglobulin receptor; EGF receptor ligand-binding  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-4660/Product: gp330 protein #status predicted <MAT>  
Query Match 5.3%; Score 11; DB 2; Length 4660;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 9 SGTCTPTQRC 19  
|||||  
Db 1147 SGTCTPTQRC 1157  
RESULT 3  
A33650  
dopamine beta-monooxygenase (EC 1.14.17.1) precursor, membrane-bound - bovine  
N:Alternate names: dopamine beta-hydroxylase  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 09-Mar-1990 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
C:Accession: A33650; A34925; JH0191; A35279; A41754; A34926; A31802; A12853  
R:Tajaniidiz, J.; Stewart, L.; Smith, A.J.; Kluman, J.P.  
Biochemistry 28, 10054-10061, 1989  
A:Title: Structure of bovine adrenal dopamine beta-monooxygenase, as deduced from cDNA a  
ptide.  
A:Reference number: A33650; MUID:90148328; PMID:2620060  
A:Accession: A33650  
A:Molecule type: mRNA  
A:Residues: 1-191, 'C', 193-266, 'RDH', 270-587, 'Q', 588-610 <TAL>  
A:Cross-references: GB:J02890  
R:Lewis, E.J.; Allison, S.; Fader, D.; Claflin, V.; Baizer, L.  
J. Biol. Chem. 265, 1021-1028, 1990  
A:Title: Bovine dopamine beta-hydroxylase cDNA. Complete coding sequence and expression  
A:Reference number: A34925; MUID:90110081; PMID:1688549  
A:Accession: A34925  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 14-610 <LE2>  
A:Cross-references: GB:J05160; NID:G162962; PIDN:AAA30490.1; PID:G162963  
R:Wu, H.J.; Farmer, R.J.; Koop, A.H.; Rozansky, D.J.; O'Connor, D.T.  
J. Neurochem. 55, 97-105, 1990  
A:Title: Molecular cloning, structure, and expression of dopamine-beta-hydroxylase from  
A:Reference number: JH0191; MUID:90285664; PMID:1693949  
A:Accession: JH0191  
A:Molecule type: mRNA  
A:Residues: 14-39, 'S', 41-103, 'D', 105-565, 'LE', 568-610 <WUH>  
A:Note: the authors translated the codon UCC for residue 40 as Phe and AAG for residue 2  
R:Wang, N.; Souchan, C.; DeWolf Jr., W.E.; Wells, T.N.C.; Kruse, L.I.; Leatherbarrow, R.  
Biochemistry 29, 6466-6474, 1990  
A:Title: Bovine dopamine beta-hydroxylase, primary structure determined by cDNA cloning  
A:Reference number: A35279; MUID:91002542; PMID:2207088  
A:Accession: A35279  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 33-348, 'R', 350-610 <WAN>  
A:Cross-references: GB:J02909  
R:Lewis, E.J.; Asnani, L.P.  
J. Biol. Chem. 267, 494-500, 1992  
A:Title: Soluble and membrane-bound forms of dopamine beta-hydroxylase are encoded by th  
A:Reference number: A41754; MUID:92112699; PMID:1730612  
A:Accession: A41754  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-76 <LEW>  
R:Robertson, J.G.; Desai, P.R.; Kumar, A.; Farrington, G.K.; Fitzpatrick, P.F.; Villafr

J. Biol. Chem. 265, 1029-1035, 1990  
A:Title: Primary amino acid sequence of bovine dopamine beta-hydroxylase.  
A:Reference number: A34926; MUID:90110082; PMID:2295597  
A:Accession: A34926  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 33-55, 'RV', 59-63, '73', 'F', 75-411, 420-441, 445-465, 468-559, 'C', 561-563, 566-603  
F:Taylor, C.S.; Kent, U.M.; Fleming, P.J.  
J. Biol. Chem. 264, 14-16, 1989  
A:Title: The membrane-binding segment of dopamine beta-hydroxylase is not an uncleaved  
A:Reference number: A31802; MUID:89079641; PMID:2909511  
A:Accession: A31802  
A:Molecule type: protein  
A:Residues: 33-37 <TAY>  
R:Skotland, T.; Ljones, T.; Flatmark, T.; Sletten, K.  
Biochem. Biophys. Res. Commun. 74, 1483-1489, 1977  
A:Title: NH-2-terminal sequence of dopamine beta-hydroxylase from bovine adrenal medull  
A:Reference number: A12853; MUID:77134133; PMID:843373  
A:Accession: A12853  
A:Molecule type: protein  
A:Residues: 33-34, 'T', 36-44, 'X', 46-47, 'TY', 50 <SKO>  
A:Experimental source: adrenal medulla  
A:Note: residue 46 was also sequenced as Ile  
R:Robertson, J.G.; Adams, G.W.; Medzihradsky, K.F.; Burlingame, A.L.; Villafranca, J.C.  
Biochemistry 33, 11563-11575, 1994  
A:Title: Complete assignment of disulfide bonds in bovine dopamine beta-hydroxylase.  
A:Reference number: A55893; MUID:95001861; PMID:7918370  
A:Contents: annotation; disulfide bonds  
C:Comment: Dopamine beta-monooxygenase catalyzes the biosynthetic conversion of dopamin  
C:Comment: Dopamine beta-monooxygenase is a tetrameric glycoprotein bound in both the  
C:Superfamily: peptidylglycine monooxygenase I homology  
C:Keywords: catecholamine biosynthesis; copper; glycoprotein; membrane protein; monooxy  
F:1-610/Product: dopamine beta-monooxygenase, membrane-bound form #status predicted <M  
F:1-32/Domain: signal sequence #link MANS #status predicted <SIG>  
F:33-610/Product: dopamine beta-monooxygenase, soluble form #status predicted <MANS>  
F:289-512/Domain: peptidylglycine monooxygenase I homology <FAM>  
F:57,177,559,604/Binding site: carboxylate (Asn) {covalent} #status predicted  
F:147-589,225-276,262-288,383-496,387-558,459-481/Disulfide bonds: #status experimental  
F:223/Active site: Tyr #status predicted  
F:237,238,255,256/Binding site: copper (His) #status predicted  
F:326,328,405,407/Binding site: copper (His) #status predicted  
F:339/Binding site: phosphate (Ser) {covalent} #status predicted  
F:521,523/Disulfide bonds: interchain #status experimental  
Query Match 3.9%; Score 8; DB 2; Length 610;  
Best Local Similarity 100.0%; Pred. No. 4.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 144 AVAVFLVI 151  
|||||  
Db 18 AVAVFLVI 25  
RESULT 4  
D89946  
protein-export membrane protein SecDF [imported] - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001  
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogi  
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsugu, K.  
Lancet 357, 1225-1240, 2001  
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A:Reference number: A89758; MUID:21311952; PMID:11418146  
A:Accession: D89946  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-759 <KUR>  
A:Cross-references: GB:BA000018; PID:gl3701435; PIDN:BA842729.1; GSPDB:GN00149  
A:Experimental source: strain N315  
C:Genetics:  
A:Gene: secF

Query Match 3.9%; Score 8; DB 2; Length 759;  
 Best Local Similarity 100.0%; Pred. No. 5.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 IVVVVAIL 160  
 |||||  
 DB 688 IVVVVAIL 695

## RESULT 5

T37190  
 neohrin - human  
 C:Species: Homo sapiens (man)  
 C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000  
 C:Accession: T37190  
 R:Kestila, M.; Lenkkeri, U.; Mannikko, M.; Lamerdin, J.; McCready, P.; Putaala, H.; Ruoto-  
 ason, K.  
 Molecular Cell 1, 575-582, 1998  
 A:Title: Positionally cloned gene for a novel glomerular protein - neohrin - is mutated  
 A:Reference number: Z21629; MUID:98325371; PMID:9660941  
 A:Accession: T37190  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1241 <RES>  
 A:Cross-references: EMBL:AF035835; NID:g3025698; PIDN:AAC39687.1; PID:g3025699  
 C:Genetics:  
 A:Gene: NPHS1  
 A:Map position: 19  
 A>Note: mutated in congenital nephrotic syndrome of the Finnish type (NPHS1); located in

Query Match 3.9%; Score 8; DB 2; Length 1241;  
 Best Local Similarity 100.0%; Pred. No. 7.9;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 SSTVSTTE 192  
 |||||  
 DB 1127 SSTVSTTE 1134

## RESULT 6

T26859  
 hypothetical protein Y43F08.3 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T26859  
 R:Ainscough, R.  
 Submitted to the EMBL Data Library, October 1998  
 A:Reference number: Z20278  
 A:Accession: T26859  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1743 <WIL>  
 A:Cross-references: EMBL:AL032623; PIDN:CAA21511.1; CESP:Y43F08.3  
 A:Experimental source: Clone Y43F8B  
 C:Genetics:  
 A:Gene: CESP:Y43F08.3  
 A:Introns: 65/1; 92/2; 128/1; 229/1; 367/1; 422/1; 496/2; 523/1; 571/1; 628/1; 857/2; 94

Query Match 3.9%; Score 8; DB 2; Length 1743;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 IPRWYNP 88  
 |||||  
 DB 89 IPRWYNP 96

## RESULT 7

A69323  
 hypothetical protein AF0585 - Archaeoglobus fulgidus  
 C:Species: Archaeoglobus fulgidus  
 C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999

C:Accession: A69323  
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
 .; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.E.  
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; McDonald, L.  
 Nature 390, 364-370, 1997  
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kaine, B.P.; Sykes, S.  
 Smith, H.O.; Woese, C.R.; Venter, J.C.  
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae  
 A:Reference number: A69250; MUID:98049343; PMID:9389475  
 C:Accession: A69323  
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-90 <KLE>  
 A:Cross-references: GB:AE001064; GB:AE000782; NID:g2689387; PIDN:AAB90659.1; PID:g26850

Query Match 3.4%; Score 7; DB 2; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 VVVVAIL 160  
 |||||  
 DB 69 VVVVAIL 75

## RESULT 8

E48338  
 hypothetical protein orf71 - equine herpesvirus 4 (strain 405/76) (fragment)  
 C:Species: equine herpesvirus 4  
 C>Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 08-Oct-1999  
 C:Accession: E48338  
 R:Nagesha, H.S.; Crabb, B.S.; Studdert, M.J.  
 Arch. Virol. 128, 143-154, 1993  
 A:Title: Analysis of the nucleotide sequence of five genes at the left end of the unig  
 A:Reference number: E48338; MUID:93119267; PMID:8380320  
 A:Accession: E48338  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-116 <NAG>  
 A:Cross-references: GB:M89634; NID:g330929; PIDN:AAA46104.1; PID:g330934  
 A>Note: sequence extracted from NCBI backbone (NCBIN:121741, NCBI:P:121746)

Query Match 3.4%; Score 7; DB 2; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 SSTVSTT 191  
 |||||  
 DB 87 SSTVSTT 93

## RESULT 9

G97172  
 hypothetical protein CAC2213 [imported] - Clostridium acetobutylicum  
 C:Species: Clostridium acetobutylicum  
 C>Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
 C:Accession: G97172  
 R:Nolling, J.; Berton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee  
 .; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
 J. Bacteriol. 183, 4823-4838, 2001  
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1  
 A:Reference number: A96900; MUID:21359325; PMID:21359325  
 A:Accession: G97172  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-135 <KUR>  
 A:Cross-references: GB:AE001437; PIDN:AAK80170.1; PID:g15025210; GSPDB:GN00168  
 A:Experimental source: Clostridium acetobutylicum ATCC824  
 C:Genetics:  
 A:Gene: CAC2213

Query Match 3.4%; Score 7; DB 2; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 KXDVFG 129  
 Db 32 KXDVFG 38

## RESULT 10

S49230  
 glycine cleavage system protein H precursor (clone HFC2) - *Flaveria cronquistii*  
 N/Alternate names: H-protein  
 C/Species: *Flaveria cronquistii*  
 C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Aug-1999  
 C/Accession: S49230; S60197  
 R/Kopriva, S.; Bauwe, H.  
 submitted to the EMBL Data Library, September 1994  
 A/Description: Molecular cloning and comparative analysis of H-protein of glycine decarboxylase  
 A/Reference number: S49229  
 A/Accession: S49230  
 A/Molecule type: DNA  
 A/Residues: 1-152 <KOP>  
 A/Cross-references: EMBL:Z37518; NID:G547518; PIDN:CAA85755.1; PID:G547519  
 R/Kopriva, S.; Bauwe, H.  
 Mol. Gen. Genet. 249, 111-116, 1995  
 A/Title: H-protein of glycine decarboxylase is encoded by multigene families in *Flaveria*  
 A/Reference number: S60194; MUID:96140454; PMID:8552027  
 A/Accession: S60197  
 A/Status: translation not shown  
 A/Molecule type: DNA  
 A/Residues: 8-148 <KOW>  
 A/Cross-references: EMBL:Z37518  
 A/Experimental source: tissue type leaf  
 C/Genetics:

A/Genome: nuclear  
 C/Superfamily: glycine cleavage system protein H; lipoyl/biotin-binding homology  
 C/Keywords: lipamide  
 F:1-31/Domain: transit peptide (mitochondrion) #status predicted <SIG>  
 F:32-152/Product: glycine cleavage system protein H #status predicted <MAT>  
 F:55-129/Domain: lipoyl/biotin-binding homology <LPB>  
 F:94/Binding site: lipamide (lys) (covalent) #status predicted

Query Match 3.4%; Score 7; DB 2; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 VDLPTDG 75  
 Db 72 VDLPTDG 78

## RESULT 11

T38729  
 hypothetical protein SPAC3G6.10c - fission yeast (*Schizosaccharomyces pombe*)  
 C/Species: *Schizosaccharomyces pombe*  
 C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 04-Mar-2000  
 C/Accession: T38729  
 R/Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
 submitted to the EMBL Data Library, September 1997  
 A/Reference number: Z21797  
 A/Accession: T38729  
 A/Status: preliminary; translated from GB/EMBL/DDBJ  
 A/Molecule type: DNA  
 A/Residues: 1-159 <GEN>  
 A/Cross-references: EMBL:Z99167; PIDN:CA16286.1; GSPDB:GN00066; SPDB:SPAC3G6.10c  
 A/Experimental source: strain 972h; cosmid C3G6  
 C/Genetics:  
 A/Gene: SPDB:SPAC3G6.10c  
 A/Map position: 1  
 C/Superfamily: *Schizosaccharomyces pombe* hypothetical protein SPAC3G6.10c

Query Match 3.4%; Score 7; DB 2; Length 159;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 SSTVSTT 191  
 Db 22 SSTVSTT 28

## RESULT 12

S60198  
 glycine cleavage system protein H precursor (clone HFP13) - *Flaveria pringlei* (fragment)  
 N/Alternate names: H-protein  
 C/Species: *Flaveria pringlei*  
 C/Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 20-Aug-1999  
 C/Accession: S60198  
 R/Kopriva, S.; Bauwe, H.  
 Mol. Gen. Genet. 249, 111-116, 1995  
 A/Title: H-protein of glycine decarboxylase is encoded by multigene families in *Flaveria*  
 A/Reference number: S60194; MUID:96140454; PMID:8552027  
 A/Accession: S60198  
 A/Status: nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-161 <KOP>  
 A/Cross-references: EMBL:Z37522; NID:G547499; PIDN:CAA85759.1; PID:G547500  
 A/Experimental source: tissue type leaf  
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1994  
 C/Genetics:

A/Genome: nuclear  
 C/Superfamily: glycine cleavage system protein H; lipoyl/biotin-binding homology  
 C/Keywords: lipamide  
 F:1-30/Domain: transit peptide (mitochondrion) (fragment) #status predicted <SIG>  
 F:31-161/Product: glycine cleavage system protein H #status predicted <MAT>  
 F:54-128/Domain: lipoyl/biotin-binding homology <LPB>  
 F:93/Binding site: lipamide (lys) (covalent) #status predicted

Query Match 3.4%; Score 7; DB 2; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 VDLPTDG 75  
 Db 71 VDLPTDG 77

## RESULT 13

A72620  
 probable NADH dehydrogenase (ubiquinone) chain 6 APE1418 - *Aeropyrum pernix* (strain KL)  
 C/Species: *Aeropyrum pernix*  
 C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Aug-1999  
 C/Accession: A72620  
 R/Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;  
 DNA Res. 6, 83-101, 1999  
 A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, *Aeropyrum pernix*  
 A/Reference number: A72450; MUID:99310339; PMID:10382966  
 A/Accession: A72620  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-173 <KAW>  
 A/Cross-references: DBJ:AP000061; NID:G5104821; PIDN:BAA80415.1; PID:dl044201; PID:G5104821  
 A/Experimental source: strain KL  
 C/Genetics:  
 A/Gene: APE1418

Query Match 3.4%; Score 7; DB 2; Length 173;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 VAVFLVI 151  
 Db 69 VAVFLVI 75

## RESULT 14

D87019  
 cytochrome C oxidase subunit III [imported] - *Mycobacterium leprae*

C:Species: Mycobacterium leprae  
 C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
 C:Accession: D87019  
 R:Coile, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H  
 R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,  
 eam, M.A.; Rutherford, K.M.  
 Nature 409, 1007-1011, 2001  
 A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S  
 A:Title: Massive gene decay in the leprosy bacillus.  
 A:Reference number: A86909; MUID:21128732; PMID:11234002  
 A:Accession: D87019  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-202 <STO>  
 A:Cross-references: GB:AL450380; NID:gl3092955; PIDN:CAC31263.1; GSPDB:GN00147  
 C:Genetics:  
 A:Gene: ctas  
 C:Superfamily: cytochrome-c oxidase chain III

Query Match	3.4%	Score 7;	DB 2;	Length 202;
Best Local Similarity	100.0%	Pred. No. 20;		
Matches	7;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;

Qy	125	DVFGRLR 131
Db	94	DVFGRLR 100

RESULT 15  
 AI3429  
 transposase BMEI1423 [imported] - Brucella melitensis (strain 16M)  
 C:Species: Brucella melitensis  
 C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002  
 C:Accession: AI3429  
 R:DelVecchio, V.G.; Kapural, V.; Redkar, R.J.; Patra, G.; Muier, C.; Los, T.; Ivanova,  
 Mazur, M.; Goltzman, E.; Seikov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes  
 Proc.Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitens  
 A:Reference number: AD3252; PMID:1175668  
 A:Accession: AI3429  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-217 <KUR>  
 A:Cross-references: GB:AE008917; PIDN:AAL52604.1; PID:gl7983423; GSPDB:GN00190  
 A:Experimental source: strain 16M  
 C:Genetics:  
 A:Gene: BMEI1423  
 A:Map position: 1

Query Match	3.4%	Score 7;	DB 2;	Length 217;
Best Local Similarity	100.0%	Pred. No. 21;		
Matches	7;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;

Qy	142	EMAVAVF 148
Db	38	EMAVAVF 44

Search completed: April 22, 2004, 10:25:49  
 Job time : 28 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2004, 10:23:45 ; Search time 361 Seconds  
(without alignments)  
157.767 Million cell updates/sec

Title: US-09-935-390A-23  
Perfect score: 206  
Sequence: 1 MERRHVCSTGCTQTPRCS.....TVSTBTEHLVYHNTPL 206

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1133595 seqs, 276475211 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : Published Applications AA:\*
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  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
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  - 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
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  - 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	100.0	206	9	US-09-935-390A-23
2	206	100.0	513	9	US-09-785-449-18
3	145	70.4	529	9	US-09-742-201-2
4	145	70.4	529	12	US-10-081-056-42
5	145	70.4	529	12	US-10-245-752-10
6	145	70.4	529	12	US-10-245-859-10
7	145	70.4	529	12	US-10-211-858-12
8	145	70.4	529	12	US-10-305-654-42
9	145	70.4	529	14	US-10-245-103-10
10	145	70.4	529	14	US-10-245-107-10
11	145	70.4	529	14	US-10-245-143-10
12	145	70.4	529	14	US-10-245-771-10
13	145	70.4	529	14	US-10-245-851-10
14	145	70.4	529	14	US-10-245-883-10
15	145	70.4	529	14	US-10-237-535-10

16	145	70.4	529	14	US-10-238-183-10	Sequence 10, Appl
17	145	70.4	529	14	US-10-238-283-10	Sequence 10, Appl
18	145	70.4	529	14	US-10-238-370-10	Sequence 10, Appl
19	145	70.4	529	14	US-10-245-055-10	Sequence 10, Appl
20	145	70.4	529	14	US-10-245-147-10	Sequence 10, Appl
21	145	70.4	529	14	US-10-245-730-10	Sequence 10, Appl
22	145	70.4	529	14	US-10-245-739-10	Sequence 10, Appl
23	145	70.4	529	14	US-10-246-210-10	Sequence 10, Appl
24	145	70.4	529	14	US-10-239-196-10	Sequence 10, Appl
25	145	70.4	529	14	US-10-243-024-10	Sequence 10, Appl
26	145	70.4	529	14	US-10-243-409-10	Sequence 10, Appl
27	145	70.4	529	14	US-10-245-621-10	Sequence 10, Appl
28	145	70.4	529	14	US-10-245-880-10	Sequence 10, Appl
29	145	70.4	529	14	US-10-245-033-10	Sequence 10, Appl
30	145	70.4	529	14	US-10-243-095-10	Sequence 10, Appl
31	145	70.4	529	14	US-10-245-185-10	Sequence 10, Appl
32	145	70.4	529	14	US-10-245-427-10	Sequence 10, Appl
33	145	70.4	529	14	US-10-245-473-10	Sequence 10, Appl
34	145	70.4	529	14	US-10-245-770-10	Sequence 10, Appl
35	145	70.4	529	14	US-10-245-877-10	Sequence 10, Appl
36	145	70.4	529	14	US-10-246-976-10	Sequence 10, Appl
37	145	70.4	529	14	US-10-243-320-10	Sequence 10, Appl
38	145	70.4	529	14	US-10-242-743-10	Sequence 10, Appl
39	145	70.4	529	14	US-10-242-845-10	Sequence 10, Appl
40	145	70.4	529	14	US-10-223-085-42	Sequence 12, Appl
41	145	70.4	529	14	US-10-237-636-10	Sequence 10, Appl
42	145	70.4	529	14	US-10-238-325-10	Sequence 10, Appl
43	145	70.4	529	14	US-10-238-346-10	Sequence 10, Appl
44	145	70.4	529	14	US-10-238-411-10	Sequence 10, Appl
45	145	70.4	529	14	US-10-243-124-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1  
US-09-935-390A-23  
; Sequence 23, Application US/09935390A  
; Patent No. US20020076761A1  
; GENERAL INFORMATION:  
; APPLICANT: Escobedo, Jaime  
; Quianjin, Hu  
; Garcia, Pablo  
; Williams, Lewis T.  
; Kothakota, Srinivas  
; TITLE OF INVENTION: Secreted Human Proteins  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/935,390A  
; FILING DATE: 22-AUG-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/988,671  
; FILING DATE: 1997-12-11  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jane E. R. Potter  
; REGISTRATION NUMBER: 33,332  
; REFERENCE/DOCKET NUMBER: 1369.002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 923-2718  
; TELEFAX: (510) 655-3542



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/
;
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 206 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: NO. US200200761A1e
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-935-390a-23

Query Match      100.0%; Score 206; DB 9; Length 206;
Best Local Similarity 100.0%; Pred. No. 8.5e-196;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCTQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKVTSGFDELQRIH 60
DB 1 MERRHPVCSGTCTQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKVTSGFDELQRIH 60
QY 61 FPSDKGHCVLDLPDTGLCKESIPRWYINPFSHCAFTYGGCYGNKNFEEBQOCLESRCRG 120
DB 61 FPSDKGHCVLDLPDTGLCKESIPRWYINPFSHCAFTYGGCYGNKNFEEBQOCLESRCRG 120
QY 121 ISKXDVFLGRREIPSTGSGVEMAVAVFLVICIVVVAIIYGVCFKQKDFHGHHP 180
DB 121 ISKXDVFLGRREIPSTGSGVEMAVAVFLVICIVVVAIIYGVCFKQKDFHGHHP 180
QY 181 PTPASSTVSTTDEHLVNHTRPL 206
DB 181 PTPASSTVSTTDEHLVNHTRPL 206

RESULT 2
US-09-765-449-18
; Sequence 18, Application US/09765449
; Patent No. US20020098537A1
; GENERAL INFORMATION:
; APPLICANT: SHIMOMURA, Takeshi
; KAWAGUCHI, Toshiya
; KITAMURA, Naomi
; MIYAZAKI, Keiji
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09765,449
; FILING DATE: 22-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,558
; FILING DATE: <Unknown>
; INFORMATION FOR SEQ ID NO: 18
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 513 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; STRAIN: MN45
; SEQUENCE DESCRIPTION: SEQ ID NO: 18
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US-09-765-449-18

Query Match      100.0%; Score 206; DB 9; Length 513;
Best Local Similarity 100.0%; Pred. No. 1.9e-195;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCTQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKVTSGFDELQRIH 60
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QY 61 FPSDKGHCVLDLPDTGLCKESIPRWYINPFSHCAFTYGGCYGNKNFEEBQOCLESRCRG 120
DB 368 FPSDKGHCVLDLPDTGLCKESIPRWYINPFSHCAFTYGGCYGNKNFEEBQOCLESRCRG 427
QY 121 ISKXDVFLGRREIPSTGSGVEMAVAVFLVICIVVVAIIYGVCFKQKDFHGHHP 180
DB 428 ISKXDVFLGRREIPSTGSGVEMAVAVFLVICIVVVAIIYGVCFKQKDFHGHHP 487
QY 181 PTPASSTVSTTDEHLVNHTRPL 206
DB 488 PTPASSTVSTTDEHLVNHTRPL 513

RESULT 3
US-09-742-201-2
; Sequence 2, Application US/09742201
; Patent No. US20020123091A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kirchhofer, Daniel K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: No. US20020123091A1e Inhibitor of Hepatocyte Growth Factor Acti
; FILE REFERENCE: P1861RIUS
; CURRENT APPLICATION NUMBER: US/09742,201
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US00/06884
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 60/253,665
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-742-201-2

Query Match      70.4%; Score 145; DB 9; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 324 MERRHPVCSGTCTQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKVTSGFDELQRIH 383
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DB 384 FPSDKGHCVLDLPDTGLCKESIPRWYINPFSHCAFTYGGCYGNKNFEEBQOCLESRCRG 443
QY 121 ISKXDVFLGRREIPSTGSGVEMAV 145
DB 444 ISKXDVFLGRREIPSTGSGVEMAV 458

RESULT 4
US-10-081-056-42
; Sequence 42, Application US/10081056
; Publication No. US2004004327A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
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APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Marsters, Scot A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Stephan, Jean-Philippe F.  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Wood, William I.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Ye, Weilian  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
 TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS  
 FILE REFERENCE: P3235P1C1  
 CURRENT APPLICATION NUMBER: US/10/081,056  
 PRIOR FILING DATE: 2002-02-20  
 PRIOR FILING DATE: 2001-07-09  
 PRIOR APPLICATION NUMBER: US 60/219,556  
 PRIOR FILING DATE: 2000-07-20  
 PRIOR APPLICATION NUMBER: US 60/220,624  
 PRIOR FILING DATE: 2000-07-25  
 PRIOR APPLICATION NUMBER: US 60/220,664  
 PRIOR FILING DATE: 2000-07-25  
 PRIOR APPLICATION NUMBER: PCT/US00/20710  
 PRIOR FILING DATE: 2000-07-28  
 PRIOR APPLICATION NUMBER: US 60/222,695  
 PRIOR FILING DATE: 2000-08-02  
 PRIOR APPLICATION NUMBER: US 09/643,657  
 PRIOR FILING DATE: 2000-08-17  
 PRIOR APPLICATION NUMBER: PCT/US00/23522  
 PRIOR FILING DATE: 2000-08-23  
 PRIOR APPLICATION NUMBER: PCT/US00/23328  
 PRIOR FILING DATE: 2000-08-24  
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 PRIOR FILING DATE: 2000-09-15  
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 PRIOR APPLICATION NUMBER: US 09/665,350  
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 PRIOR FILING DATE: 2000-11-08  
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 PRIOR FILING DATE: 2000-11-08  
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 PRIOR FILING DATE: 2000-11-10  
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 PRIOR FILING DATE: 2000-12-01  
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 PRIOR FILING DATE: 2000-12-20  
 PRIOR APPLICATION NUMBER: PCT/US00/34956  
 PRIOR FILING DATE: 2000-12-20  
 PRIOR APPLICATION NUMBER: US 09/767,609  
 PRIOR FILING DATE: 2001-01-22  
 PRIOR APPLICATION NUMBER: US 09/796,498  
 PRIOR FILING DATE: 2001-02-28  
 PRIOR APPLICATION NUMBER: PCT/US01/06520  
 PRIOR FILING DATE: 2001-02-28  
 PRIOR APPLICATION NUMBER: PCT/US01/06666  
 PRIOR FILING DATE: 2001-03-01  
 PRIOR APPLICATION NUMBER: US 09/802,706  
 PRIOR FILING DATE: 2001-03-09  
 PRIOR APPLICATION NUMBER: US 09/808,689  
 PRIOR FILING DATE: 2001-03-14  
 PRIOR APPLICATION NUMBER: US 09/816,744  
 PRIOR FILING DATE: 2001-03-22

PRIOR APPLICATION NUMBER: US 09/828,366  
 PRIOR FILING DATE: 2001-04-05  
 PRIOR APPLICATION NUMBER: US 09/854,208  
 PRIOR FILING DATE: 2001-05-10  
 PRIOR APPLICATION NUMBER: US 09/854,280  
 PRIOR FILING DATE: 2001-05-10  
 PRIOR APPLICATION NUMBER: US 09/866,028  
 PRIOR FILING DATE: 2001-05-25  
 PRIOR APPLICATION NUMBER: US 09/866,034  
 PRIOR FILING DATE: 2001-05-25  
 PRIOR APPLICATION NUMBER: PCT/US01/17092  
 PRIOR FILING DATE: 2001-05-25  
 PRIOR APPLICATION NUMBER: US 09/870,574  
 PRIOR FILING DATE: 2001-05-30  
 PRIOR APPLICATION NUMBER: PCT/US01/17443  
 PRIOR FILING DATE: 2001-05-30  
 PRIOR APPLICATION NUMBER: PCT/US01/17800  
 PRIOR FILING DATE: 2001-06-01  
 PRIOR APPLICATION NUMBER: PCT/US01/19692  
 PRIOR FILING DATE: 2001-06-20  
 PRIOR APPLICATION NUMBER: PCT/US01/00000  
 PRIOR FILING DATE: 2001-06-28  
 NUMBER OF SEQ ID NOS: 383  
 SEQ ID NO 42  
 LENGTH: 529  
 TYPE: PRT  
 ORGANISM: Homosapiens  
 US-10-081-056-42  
 Query Match 70.4%; Score 145; DB 12; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-135;  
 Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MERRHPVCSGTCTOPTGRCNGCCIDSFLECDTNCPCDASDAACEKYTSGFDELQRIH 60  
 Db 324 MERRHPVCSGTCTOPTGRCNGCCIDSFLECDTNCPCDASDAACEKYTSGFDELQRIH 383  
 Qy 61 FPSDKGHCVDLPDTGLCKESIPRWYNNPFSHCARFTYGCYGNKNNFEEQCLSCRG 120  
 Db 384 FPSDKGHCVDLPDTGLCKESIPRWYNNPFSHCARFTYGCYGNKNNFEEQCLSCRG 443  
 Qy 121 ISKQVFLRLRREIPISTGSEMAV 145  
 Db 444 ISKQVFLRLRREIPISTGSEMAV 468  
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 US-10-245-752-10  
 Sequence 10, Application US/10245752  
 Publication No. US20030064473A1  
 GENERAL INFORMATION:  
 APPLICANT: Baker, Kevin  
 APPLICANT: Eaton, Dan  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin  
 APPLICANT: Smith, Victoria  
 APPLICANT: Stephan, Jean-Philippe  
 APPLICANT: Watanabe, Colin  
 APPLICANT: Wood, William  
 APPLICANT: Zhang, Zemin  
 APPLICANT: Pong, Sherman  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ACIDS ENCODING THE SAME  
 FILE REFERENCE: P3630RIC66  
 CURRENT APPLICATION NUMBER: US/10/245,752  
 CURRENT FILING DATE: 2002-09-16  
 PRIOR APPLICATION NUMBER: 10/197942  
 PRIOR FILING DATE: 2002-07-18  
 PRIOR APPLICATION NUMBER: 60/059114  
 PRIOR FILING DATE: 1997-09-17  
 PRIOR APPLICATION NUMBER: 60/063046

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; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 10
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-752-10

Query Match          70.4%; Score 145; DB 12; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTNPDPASDEAAACEKYTSGFDELQRIH 60
Db 324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTNPDPASDEAAACEKYTSGFDELQRIH 383
QY 61 FPSDKGHCVLDPTGLCKESIPRWYNPFSEHCARFTYGGCYGNKNPFEEBQQCLESRCG 120
Db 384 FPSDKGHCVLDPTGLCKESIPRWYNPFSEHCARFTYGGCYGNKNPFEEBQQCLESRCG 443
QY 121 ISKDVFGRLRREIPIPTSGSVMNAV 145
Db 444 ISKDVFGRLRREIPIPTSGSVMNAV 468

RESULT 6
US-10-245-859-10
; Sequence 10, Application US/10245859
; Publication No. US20030064474A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630RAC78
; CURRENT APPLICATION NUMBER: US/10/245,859
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478

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; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 10
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-859-10

Query Match          70.4%; Score 145; DB 12; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTNPDPASDEAAACEKYTSGFDELQRIH 60
Db 324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTNPDPASDEAAACEKYTSGFDELQRIH 383
QY 61 FPSDKGHCVLDPTGLCKESIPRWYNPFSEHCARFTYGGCYGNKNPFEEBQQCLESRCG 120
Db 384 FPSDKGHCVLDPTGLCKESIPRWYNPFSEHCARFTYGGCYGNKNPFEEBQQCLESRCG 443
QY 121 ISKDVFGRLRREIPIPTSGSVMNAV 145
Db 444 ISKDVFGRLRREIPIPTSGSVMNAV 468

RESULT 7
US-10-211-858-12
; Sequence 12, Application US/10211858
; Publication No. US20030211096A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Pitti, Robert M.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stone, Donna M.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P293IRIC1
; CURRENT APPLICATION NUMBER: US/10/211,858
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/014699
; PRIOR FILING DATE: 1996-04-01
; PRIOR APPLICATION NUMBER: 60/026943
; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 60/059121
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/062037
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/066511

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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 258
; SEQ ID NO 12
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-858-12

Query Match          70.4%; Score 145; DB 12; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MERRHPVCSGTCTQPTQRCNSGCCIDSFLECDTTPNCPDASDEAAACEKTYSGFDELQRIH 60
Db 324 MERRHPVCSGTCTQPTQRCNSGCCIDSFLECDTTPNCPDASDEAAACEKTYSGFDELQRIH 383

Qy 61 FPSDKGHCVDLPDTGLCKESI PRWYNNPFSFHCARFTYGGCYGNKNPFEEQQCLSCRG 120
Db 384 FPSDKGHCVDLPDTGLCKESI PRWYNNPFSFHCARFTYGGCYGNKNPFEEQQCLSCRG 443

Qy 121 ISKXDVFLRLREIPIPTSGVEMAV 145
Db 444 ISKXDVFLRLREIPIPTSGVEMAV 468

RESULT 8
US-10-305-654-42
; Sequence 42, Application US/10305654
; Publication No. US20030224984A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Gerber, Hans-Peter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Masters, Scot A.
; APPLICANT: Pan, J.
; APPLICANT: Paoni, N. F.
; APPLICANT: Stephan, J-P. F.
; APPLICANT: Watanabe, C.K.
; APPLICANT: Wood, W.I.
; APPLICANT: Williams, P.M.
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235RIC1
; CURRENT APPLICATION NUMBER: US/10/305,654
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 42
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homosapiens
US-10-305-654-42

Query Match          70.4%; Score 145; DB 12; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MERRHPVCSGTCTQPTQRCNSGCCIDSFLECDTTPNCPDASDEAAACEKTYSGFDELQRIH 60
Db 324 MERRHPVCSGTCTQPTQRCNSGCCIDSFLECDTTPNCPDASDEAAACEKTYSGFDELQRIH 383

Qy 61 FPSDKGHCVDLPDTGLCKESI PRWYNNPFSFHCARFTYGGCYGNKNPFEEQQCLSCRG 120
Db 384 FPSDKGHCVDLPDTGLCKESI PRWYNNPFSFHCARFTYGGCYGNKNPFEEQQCLSCRG 443
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Qy 121 ISKXDVFLRLREIPIPTSGVEMAV 145
Db 444 ISKXDVFLRLREIPIPTSGVEMAV 468

RESULT 9
US-10-245-103-10
; Sequence 10, Application US/10245103
; Publication No. US20030068778A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Pong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630RIC112
; CURRENT APPLICATION NUMBER: US/10/245,103
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 10
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-103-10

Query Match          70.4%; Score 145; DB 14; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MERRHPVCSGTCTQPTQRCNSGCCIDSFLECDTTPNCPDASDEAAACEKTYSGFDELQRIH 60
Db 324 MERRHPVCSGTCTQPTQRCNSGCCIDSFLECDTTPNCPDASDEAAACEKTYSGFDELQRIH 383

Qy 61 FPSDKGHCVDLPDTGLCKESI PRWYNNPFSFHCARFTYGGCYGNKNPFEEQQCLSCRG 120
Db 384 FPSDKGHCVDLPDTGLCKESI PRWYNNPFSFHCARFTYGGCYGNKNPFEEQQCLSCRG 443

Qy 121 ISKXDVFLRLREIPIPTSGVEMAV 145
Db 444 ISKXDVFLRLREIPIPTSGVEMAV 468

RESULT 10
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US-10-245-107-10  
; Sequence 10, Application US/10245107  
; Publication No. US20030068779A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C71  
; CURRENT APPLICATION NUMBER: US/10/245,107  
; PRIOR FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 10  
; LENGTH: 529  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-245-107-10

Query Match 70.4%; Score 145; DB 14; Length 529;  
Best Local Similarity 100.0%; Pred. No. 5.3e-135; Indels 0; Gaps 0;  
Matches 145; Conservative 0; Mismatches 0;  
QY 1 MERRHPVCSGTQPTQFRCSNGCCIDSFLECDTTPNCPDASDEAAACEKYTSGFDELQRIH 60  
DB 324 MERRHPVCSGTQPTQFRCSNGCCIDSFLECDTTPNCPDASDEAAACEKYTSGFDELQRIH 383  
QY 61 FPSDKGHCVLPTGLCKESIPIRWYNNPSEHCARFTYGGCYGNKNPFEEQOCLESRG 120  
DB 384 FPSDKGHCVLPTGLCKESIPIRWYNNPSEHCARFTYGGCYGNKNPFEEQOCLESRG 443  
QY 121 ISKQDVFGLRRRPIPTSGVEMAV 145  
DB 444 ISKQDVFGLRRRPIPTSGVEMAV 468  
RESULT 11  
US-10-245-143-10  
; Sequence 10, Application US/10245143  
; Publication No. US20030068780A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan

APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Phillippe  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C90  
CURRENT APPLICATION NUMBER: US/10/245,143  
CURRENT FILING DATE: 2002-09-16  
PRIOR APPLICATION NUMBER: 10/197942  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 10  
LENGTH: 529  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-245-143-10  
Query Match 70.4%; Score 145; DB 14; Length 529;  
Best Local Similarity 100.0%; Pred. No. 5.3e-135; Indels 0; Gaps 0;  
Matches 145; Conservative 0; Mismatches 0;  
QY 1 MERRHPVCSGTQPTQFRCSNGCCIDSFLECDTTPNCPDASDEAAACEKYTSGFDELQRIH 60  
DB 324 MERRHPVCSGTQPTQFRCSNGCCIDSFLECDTTPNCPDASDEAAACEKYTSGFDELQRIH 383  
QY 61 FPSDKGHCVLPTGLCKESIPIRWYNNPSEHCARFTYGGCYGNKNPFEEQOCLESRG 120  
DB 384 FPSDKGHCVLPTGLCKESIPIRWYNNPSEHCARFTYGGCYGNKNPFEEQOCLESRG 443  
QY 121 ISKQDVFGLRRRPIPTSGVEMAV 145  
DB 444 ISKQDVFGLRRRPIPTSGVEMAV 468  
RESULT 12  
US-10-245-771-10  
; Sequence 10, Application US/10245771  
; Publication No. US20030068781A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe

```
; APPLICANT: Watanbe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C98
; CURRENT APPLICATION NUMBER: US/10/245,771
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 10
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-245-771-10

Query Match 70.4%; Score 145; DB 14; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MERRHPVCSGTCTPTGCKESIPRWYNPFSEHCARFTYGCYGNKNFEEQQLSCRG 60
D5 324 MERRHPVCSGTCTPTGCKESIPRWYNPFSEHCARFTYGCYGNKNFEEQQLSCRG 383
Qy 61 FPSDKGHCVDLPDTGLCKESIPRWYNPFSEHCARFTYGCYGNKNFEEQQLSCRG 120
D5 384 FPSDKGHCVDLPDTGLCKESIPRWYNPFSEHCARFTYGCYGNKNFEEQQLSCRG 443
Qy 121 ISKDVFGRLRRRPIPTSGVEMAV 145
D5 444 ISKDVFGRLRRRPIPTSGVEMAV 468

RESULT 13
US-10-245-851-10
; Sequence 10, Application US/10245851
; Publication No. US20030068782A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanbe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C70
; CURRENT APPLICATION NUMBER: US/10/245,883
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
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; FILE REFERENCE: P3630R1C93
; CURRENT APPLICATION NUMBER: US/10/245,851
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 10
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-245-851-10

Query Match 70.4%; Score 145; DB 14; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MERRHPVCSGTCTPTGCKESIPRWYNPFSEHCARFTYGCYGNKNFEEQQLSCRG 60
D5 324 MERRHPVCSGTCTPTGCKESIPRWYNPFSEHCARFTYGCYGNKNFEEQQLSCRG 383
Qy 61 FPSDKGHCVDLPDTGLCKESIPRWYNPFSEHCARFTYGCYGNKNFEEQQLSCRG 120
D5 384 FPSDKGHCVDLPDTGLCKESIPRWYNPFSEHCARFTYGCYGNKNFEEQQLSCRG 443
Qy 121 ISKDVFGRLRRRPIPTSGVEMAV 145
D5 444 ISKDVFGRLRRRPIPTSGVEMAV 468

RESULT 14
US-10-245-883-10
; Sequence 10, Application US/10245883
; Publication No. US20030068783A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanbe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C70
; CURRENT APPLICATION NUMBER: US/10/245,883
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
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PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091358
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/106932
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/115554
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119342
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/123957
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123972
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: 60/127372
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PRIOR APPLICATION NUMBER: 60/131271
PRIOR FILING DATE: 1999-04-27
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PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138385
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PRIOR FILING DATE: 1999-07-20
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PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144790
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145228
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146943
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PRIOR APPLICATION NUMBER: 60/149327
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149395
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/150114
PRIOR FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: 60/151700
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/151734
PRIOR FILING DATE: 1999-08-31

PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
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PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091358
PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1999-07-28
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PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/151734
PRIOR FILING DATE: 1999-08-31

Query Match 70.4%; Score 145; DB 14; Length 529;
Best Local Similarity 100.0%; Pred No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHVCSTQPTQFRCSNGCCIDSFLECDTNPDPASDEACEKYTSGFDELQRIH 60
324 MERRHVCSTQPTQFRCSNGCCIDSFLECDTNPDPASDEACEKYTSGFDELQRIH 383
QY 61 FPDKGHCVDLPDGLCKESIPRWYNNPSEHCARFTYGGCYGNKNFEEEOCLSCRG 120
384 FPDKGHCVDLPDGLCKESIPRWYNNPSEHCARFTYGGCYGNKNFEEEOCLSCRG 443
QY 121 ISKQVFLGRLRREIPSTGSVENAV 145
444 ISKQVFLGRLRREIPSTGSVENAV 468

RESULT 15
US-10-237-535-10
Sequence 10, Application US/10237535
Publication No. US20030073188A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C3
CURRENT APPLICATION NUMBER: US/10/237,535
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689

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 / PRIOR APPLICATION NUMBER: 10/052586  
 / PRIOR FILING DATE: 2002-01-15  
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 / PRIOR FILING DATE: 2002-02-20  
 / PRIOR APPLICATION NUMBER: 10/119480  
 / PRIOR FILING DATE: 2003-04-09

Query Match 70.4%; Score 145; DB 14; Length 529;

Best Local Similarity 100.0%; Pred. No. 5.3e-135; Indels 0; Gaps 0;  
Matches 145; Conservative 0; Mismatches 0;

QY	1	MERRHVCVSGTCQPTQFRCSGCCIDSFLECDTNCPCDASDEAAACEKTSFDELQRIH	60
DB	324	MERRHVCVSGTCQPTQFRCSGCCIDSFLECDTNCPCDASDEAAACEKTSFDELQRIH	383
QY	61	PFSDKGHCVDLPDTGLCKESIPRWYNNPSEHCABTYGGCYGNKNFEEEOCLESRG	120
DB	384	PFSDKGHCVDLPDTGLCKESIPRWYNNPSEHCABTYGGCYGNKNFEEEOCLESRG	443
QY	121	ISKDVFGLRRRPIPISTGSVEMAV	145
DB	444	ISKDVFGLRRRPIPISTGSVEMAV	468

Search completed: April 22, 2004, 10:32:27  
Job time : 362 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 22, 2004, 08:30:04 ; Search time 70 seconds  
(without alignments)  
831.497 Million cell updates/sec

Title: US-09-935-390A-23

Perfect score: 206

Sequence: 1 MERRHPVCSGCTQTPRCS.....TVSTTTEHLVYNTTRPL 206

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A Geneseq 29Jan04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1980s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	206	100.0	206	2 AAW63684	AAW63684 Human sec
2	206	100.0	348	3 AAO17713	AAO17713 Human pro
3	206	100.0	348	3 AAO17718	AAO17718 Human pro
4	206	100.0	513	2 AAW27368	AAW27368 Hepatocyte
5	206	100.0	513	2 AAW27363	AAW27363 Human HAI
6	157	76.2	487	6 ABU92043	ABU92043 Human pro
7	145	70.4	529	4 AAB20113	AAB20113 Human imm
8	145	70.4	529	4 AAO93332	AAO93332 Human pro
9	145	70.4	529	5 AAU86133	AAU86133 Human pro
10	145	70.4	529	5 ABB84837	ABB84837 Human pro
11	145	70.4	529	5 ABG34034	ABG34034 Human pro
12	145	70.4	529	5 ABB95443	ABB95443 Human ang
13	145	70.4	529	6 ADA01278	ADA01278 Human pro
14	145	70.4	529	6 ADA43707	ADA43707 Human sec
15	145	70.4	529	6 ADA43475	ADA43475 Human sec
16	145	70.4	529	6 ADA01150	ADA01150 Human pro
17	145	70.4	529	7 ADA01034	ADA01034 Human sec
18	145	70.4	529	7 ADA43591	ADA43591 Human pro
19	145	70.4	529	7 ADA06853	ADA06853 Human pro
20	145	70.4	529	7 ADA08341	ADA08341 Novel hum
21	145	70.4	529	7 ADB99634	ADB99634 Human pro
22	145	70.4	529	7 ADB86917	ADB86917 Human pro
23	145	70.4	529	7 ADB66072	ADB66072 Human pro
24	145	70.4	529	7 ADB99750	ADB99750 Human pro
25	145	70.4	529	7 ADB99405	ADB99405 Novel hum

26	145	70.4	529	7 ADB65956	ADB65956 Human sec
27	145	70.4	529	7 ADC23354	ADC23354 Human tra
28	145	70.4	529	7 ADC26047	ADC26047 Human pro
29	145	70.4	529	7 ADD10331	ADD10331 Human sec
30	145	70.4	529	7 ADD11291	ADD11291 Human sec
31	145	70.4	529	7 ADD37084	ADD37084 Human sec
32	145	70.4	529	7 ADE04874	ADE04874 Human pro
33	145	70.4	529	7 ADE11180	ADE11180 Human pro
34	145	70.4	529	7 ADD88111	ADD88111 Human pro
35	145	70.4	529	7 ADD95406	ADD95406 Human sec
36	145	70.4	529	7 ADE06336	ADE06336 Human pro
37	145	70.4	529	7 ADE38111	ADE38111 Human pro
38	145	70.4	529	7 ADD88227	ADD88227 Human pro
39	145	70.4	529	7 ADD90808	ADD90808 Human sec
40	145	70.4	529	8 ADE51661	ADE51661 Human sec
41	145	70.4	529	8 ADE51777	ADE51777 Human sec
42	145	70.4	529	8 ADE37635	ADE37635 Human sec
43	145	70.4	529	8 ADE37519	ADE37519 Human sec
44	145	70.4	529	8 ADD95290	ADD95290 Human sec
45	145	70.4	529	8 ADE37990	ADE37990 Human pro

#### ALIGNMENTS

RESULT 1  
AAW63684  
ID AAW63684 standard; protein; 206 AA.

XX AC AAW63684;

DT 24-SEP-1998 (first entry)

XX DE Human secreted protein 4.

XX KW Secreted protein; human; cell proliferation; cytokine activity;  
XX KW tissue growth; cellular differentiation; regeneration; activin; inhibin;  
XX KW chemotactic; haemostatic; thrombolytic; tumour inhibition;  
XX KW anti-inflammatory activity; biomarker.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX PT Domain 68..122

XX PT /note= "kunitz type serine protease inhibitor domain"

XX PN WO9825959-A2.

XX PD 18-JUN-1998.

XX PF 11-DEC-1997; 97WO-US023787.

XX PR 11-DEC-1996; 96US-0032757P.

XX PA (CHIR ) CHIRON CORP.

XX PI Escobedo J, Hu Q, Garcia P, Williams LT, Kothakota S;

XX DR WPI: 1998-348453/30.

XX DR N-PSDB; AAV43604.

XX PT Secreted human polypeptides - having cytokine, cell proliferation or  
XX PT differentiation, activin or inhibin, tumour inhibition or anti-  
XX PT inflammatory activities.

XX PS Claim 1; Page 52; 78pp; English.

XX CC This represents a human secreted protein. The specification provides  
XX CC secreted protein sequences (AAW63681 to AAW63699) encoded by the nucleic  
XX CC acid sequences shown in AAV43601 to AAV43619. The invention provides a  
XX CC method of identifying a secreted polypeptide which is modified by rough  
XX CC microsomes. The secreted proteins can be used in assays to determine  
XX CC biological activities, such as cytokine, cell proliferation, or cellular

CC differentiation activities, tissue growth or regeneration, activin or  
 CC inhibin activity, chemotactic or chemokinetic activity, haemostatic or  
 CC thrombolytic activity, receptor/ligand activity, tumour inhibition, or  
 CC anti-inflammatory activity. The proteins can also be used as biomarkers,  
 CC to identify tissues or cell types which express the proteins, or a stage-  
 CC or disease-specific alteration in protein expression. They can be used in  
 CC protein interaction assays, to identify ligands or binding proteins.  
 CC Compounds which affect the biological activities of the secreted proteins  
 CC or their ability to interact with specific ligands can be identified  
 CC using the proteins in screening assays. The proteins and antibodies that  
 CC bind specifically to the protein can also be used to design diagnostic  
 CC tests and therapeutic compositions for diseases which may be associated  
 CC with altered expression of these proteins. Fusion proteins comprising,  
 CC e.g. signal sequences or transmembrane domains of the proteins can be  
 CC used to target other protein domains to cellular membrane or they can be  
 CC secreted extracellularly  
 XX  
 SQ Sequence 206 AA;  
 Query Match 100.0%; Score 206; DB 2; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-198;  
 Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MERRHPVCSGTQPTQFCNSGCCIDSFLECDTTPNCPSDEACEKVTSGFDELQRIH 60  
 DB 1 MERRHPVCSGTQPTQFCNSGCCIDSFLECDTTPNCPSDEACEKVTSGFDELQRIH 60  
 QY 61 FPSDKGHCVDLPDTGLCKESIPRWYYPFSEHCARFTYGGYGNKNFEEQOCLESRG 120  
 DB 61 FPSDKGHCVDLPDTGLCKESIPRWYYPFSEHCARFTYGGYGNKNFEEQOCLESRG 120  
 QY 121 ISKXDVFLGLRRRIPSTGSEVMAVAVFLVICIVVVAILGYCFFKNQKDFHGHHP 180  
 DB 121 ISKXDVFLGLRRRIPSTGSEVMAVAVFLVICIVVVAILGYCFFKNQKDFHGHHP 180  
 QY 181 PTPASSTVSTTETDEHLVYNHTTPL 206  
 DB 181 PTPASSTVSTTETDEHLVYNHTTPL 206  
 RESULT 2  
 ID AA017713 standard; protein; 348 AA.  
 XX  
 AC AA017713;  
 XX  
 DT 08-AUG-2002 (first entry)  
 XX  
 DE Human protease associated protein HPRAP-2.  
 XX  
 KW Human; protease associated protein; HPRAP; cancer; inflammation;  
 KW anti-HIV; antianemic; antiarteriosclerotic; antidiabetic; cytostatic;  
 KW antiinflammatory; hepatotropic; antidiabetic; nephrotropic; antigout;  
 KW antithyroid; immunosuppressive; thyromimetic; virucide; dermatological;  
 KW neuroprotective; cardiac; osteopathic; antiarthritic; antiparasitic;  
 KW antipsoriatic; uropathic; ophthalmological; antirheumatic; tranquiliser;  
 KW vulnary; antiulcer; immune disorder; gene therapy; HPRAP-2.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9957274-A1.  
 XX  
 PD 11-NOV-1999.  
 XX  
 PF 28-APR-1999; 99WO-US009190.  
 XX  
 PR 01-MAY-1998; 98US-00071709.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Hillman JL, Tang YT, Lal P, Corley NC, Guegler KJ, Patterson C;  
 XX  
 XX WPI; 2000-062147/05.  
 DR

DR N-PSDB; AAL46725.  
 XX  
 PT Novel human protease associated proteins used for, e.g. the diagnosis and  
 PT prevention of cell proliferative and immune disorders.  
 XX  
 XX Claim 1; Page; 75pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of four  
 CC human protease associated proteins, designated HPRAP-1, HPRAP-2, HPRAP-3  
 CC and HPRAP-4. Human protease associated proteins are expressed in cancer  
 CC and immortalised cell lines and tissues associated with inflammation and  
 CC the immune response, and so appear to play a role in cell proliferative  
 CC and immune disorders. The sequences can be used to diagnose, treat or  
 CC prevent cell proliferative and immune disorders, including actinic  
 CC keratosis, arteriosclerosis, atherosclerosis, myelofibrosis, paroxysmal  
 CC hepatitis, mixed connective tissue disease, bursitis, cirrhosis,  
 CC thrombocythaemia, polycythaemia vera, psoriasis, primary  
 CC nocturnal haemoglobinuria, Addison's disease, adult respiratory distress  
 CC syndrome, allergies, ankylosing spondylitis, amyloidosis, anaemia,  
 CC asthma, atherosclerosis, autoimmune haemolytic anaemia, autoimmune  
 CC thyroiditis, bronchitis, cholecystitis, contact dermatitis, Crohn's  
 CC disease, atopic dermatitis, dermatomyositis, diabetes mellitus,  
 CC emphysema, episodic lymphopenia with lymphocytotoxicity, erythroblastosis  
 CC fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis,  
 CC Goodpasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis,  
 CC hyperesinophilia, irritable bowel syndrome, multiple sclerosis,  
 CC myasthenia gravis, myocardial or pericardial inflammation,  
 CC osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis,  
 CC Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjogren's syndrome,  
 CC systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis,  
 CC thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome,  
 CC infections and trauma. The present sequence is the HPRAP-2 protein. Note:  
 CC The present sequence is not obtainable from this Derwent basic but was  
 CC obtained from the Derwent family equivalent US6171790  
 XX  
 SQ Sequence 348 AA;  
 Query Match 100.0%; Score 206; DB 3; Length 348;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-198;  
 Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MERRHPVCSGTQPTQFCNSGCCIDSFLECDTTPNCPSDEACEKVTSGFDELQRIH 60  
 DB 143 MERRHPVCSGTQPTQFCNSGCCIDSFLECDTTPNCPSDEACEKVTSGFDELQRIH 202  
 QY 61 FPSDKGHCVDLPDTGLCKESIPRWYYPFSEHCARFTYGGYGNKNFEEQOCLESRG 120  
 DB 203 FPSDKGHCVDLPDTGLCKESIPRWYYPFSEHCARFTYGGYGNKNFEEQOCLESRG 262  
 QY 121 ISKXDVFLGLRRRIPSTGSEVMAVAVFLVICIVVVAILGYCFFKNQKDFHGHHP 180  
 DB 263 ISKXDVFLGLRRRIPSTGSEVMAVAVFLVICIVVVAILGYCFFKNQKDFHGHHP 322  
 QY 181 PTPASSTVSTTETDEHLVYNHTTPL 206  
 DB 323 PTPASSTVSTTETDEHLVYNHTTPL 348  
 RESULT 3  
 ID AA017718 standard; protein; 348 AA.  
 XX  
 AC AA017718;  
 XX  
 DT 08-AUG-2002 (first entry)  
 XX  
 DE Human protease associated protein HPRAP-2.  
 XX  
 KW Human; protease associated protein; HPRAP; cancer; inflammation;  
 KW anti-HIV; antianemic; antiarteriosclerotic; antidiabetic; cytostatic;  
 KW antiinflammatory; hepatotropic; antidiabetic; nephrotropic; antigout;  
 KW antithyroid; immunosuppressive; thyromimetic; virucide; dermatological;  
 KW neuroprotective; cardiac; osteopathic; antiarthritic; antiparasitic;  
 KW antipsoriatic; uropathic; ophthalmological; antirheumatic; tranquiliser;  
 KW vulnary; antiulcer; immune disorder; gene therapy; HPRAP-2.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9957274-A1.  
 XX  
 PD 11-NOV-1999.  
 XX  
 PF 28-APR-1999; 99WO-US009190.  
 XX  
 PR 01-MAY-1998; 98US-00071709.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Hillman JL, Tang YT, Lal P, Corley NC, Guegler KJ, Patterson C;  
 XX  
 XX WPI; 2000-062147/05.  
 DR

KW antipsoriatic; uropathic; ophthalmological; antirheumatic; tranquiliser;  
KW vulnery; antituler; immune disorder; gene therapy; HPRAP-2.  
XX Homo sapiens.  
XX WO9957274-A1.  
XX 11-NOV-1999.  
XX 28-APR-1999; 99WO-US009190.  
XX 01-MAY-1998; 98US-00071709.  
XX (INCY-) INCYTE PHARM INC.  
XX Hillman JL, Tang YT, Lal P, Corley NC, Guegler KJ, Patterson C;  
XX WPI; 2000-062147/05.  
XX Novel human protease associated proteins used for, e.g. the diagnosis and  
XX prevention of cell proliferative and immune disorders.  
XX Disclosure; Page: 75pp; English.  
XX The present invention provides the protein and coding sequences of four  
XX human protease associated proteins, designated HPRAP-1, HPRAP-2, HPRAP-3  
XX and HPRAP-4. Human protease associated proteins are expressed in cancer  
XX and immortalised cell lines and tissues associated with inflammation and  
XX the immune response, and so appear to play a role in cell proliferative  
XX and immune disorders. The sequences can be used to diagnose, treat or  
XX prevent cell proliferative and immune disorders, including actinic  
XX keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis,  
XX hepatitis, mixed connective tissue disease, myelofibrosis, paroxysmal  
XX nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary  
XX thrombocythaemia, AIDS, Addison's disease, adult respiratory distress  
XX syndrome, allergies, ankylosing spondylitis, amyloidosis, anaemia,  
XX asthma, atherosclerosis, autoimmune haemolytic anaemia, autoimmune  
XX thyroiditis, bronchitis, cholecystitis, contact dermatitis, Crohn's  
XX disease, atopic dermatitis, dermatomyositis, diabetes mellitus,  
XX emphysema, episodic lymphopenia with lymphocytotoxicity, erythroblastosis  
XX fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis,  
XX Goodpasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis,  
XX hyper eosinophilia, irritable bowel syndrome, multiple sclerosis,  
XX myasthenia gravis, myocardial or pericardial inflammation,  
XX osteoarthritis, osteoporosis, pancreatitis, polyomyelitis, psoriasis,  
XX Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjogren's syndrome,  
XX systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis,  
XX thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome,  
XX infections and trauma. The present sequence is the HPRAP-2 protein, which  
XX was used in a homology comparison in the exemplification of the  
XX invention. Note: The present sequence was not obtainable from this  
XX Derwent basic but was obtained from the Derwent family equivalent  
XX US6171790  
XX  
XX Sequence 348 AA;  
Query Match 100.0%; Score 206; DB 3; Length 348;  
Best Local Similarity 100.0%; Pred. No. 3.9e-198;  
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MERRHPVCSCTGCTQPTQRCNSGCCIDSLFECDDTNCPCDASDEAAACEKYTSFGDELQRIH 60  
DB 143 MERRHPVCSCTGCTQPTQRCNSGCCIDSLFECDDTNCPCDASDEAAACEKYTSFGDELQRIH 202  
QY 61 FPSDKGHCVLDLPTDGLCKESIPRWYNNPFSEHCARFTYGGCYGNKNFEEQQCLSCRG 120  
DB 203 FPSDKGHCVLDLPTDGLCKESIPRWYNNPFSEHCARFTYGGCYGNKNFEEQQCLSCRG 262  
QY 121 ISKQDVFGLRREIPSTGSGVEMAVFLVICVWVAILGYCFFKNQKDFGHHHPP 180  
DB 263 ISKQDVFGLRREIPSTGSGVEMAVFLVICVWVAILGYCFFKNQKDFGHHHPP 322  
QY 181 PTPASSTVSTTETEDTEHLVYNHTRPL 206

DB 323 PTPASSTVSTTETEDTEHLVYNHTRPL 348  
RESULT 4  
AAW27368  
ID AAW27368 standard; protein; 513 AA.  
XX  
XX AAW27368;  
XX  
XX 21-NOV-1997 (first entry)  
XX  
XX Hepatocyte growth factor activator inhibitor.  
XX  
XX Inhibition; inhibitor; protease; hepatocyte; growth factor; activation;  
XX activator; human; cancer; cell line; MKM45; regulation; regulator;  
XX antibody; kinetic study; assay standard.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX FT Peptide 1..35  
XX FT Peptide /label= sig\_peptide  
XX FT Peptide 36..513  
XX FT Peptide /label= mat\_peptide  
XX  
XX EP759467-A2.  
XX  
XX 26-FEB-1997.  
XX  
XX 23-JUL-1996; 96EP-00111870.  
XX  
XX 24-JUL-1995; 95JP-00187135.  
XX (MITU ) MITSUBISHI CHEM CORP.  
XX Shimomura T, Kawaguchi T, Kitamura N, Miyazawa K;  
XX WPI; 1997-147516/14.  
XX N-PSDB; AAT90038.  
XX  
XX New hepatocyte growth factor activator inhibitor and DNA - regulates  
XX hepatocyte growth factor and/or HGF activator in vivo or in vitro, and  
XX are used in kinetic studies.  
XX  
XX Claim 3; Page 28-30; 38pp; English.  
XX  
XX The present sequence is an inhibitor of the protease activity of  
XX hepatocyte growth factor (HGF) activator (HGFA), which has a molecular  
XX weight of about 40 kD when determined by SDS-PAGE. The inhibitor, which  
XX was isolated from the human cancer cell line MKM45, can be used as an in  
XX vivo or in vitro regulatory factor for HGF or HGFA. It can also be used  
XX to raise antibodies, useful in kinetic studies of the inhibitor, or as  
XX assay standards  
XX  
XX Sequence 513 AA;  
Query Match 100.0%; Score 206; DB 2; Length 513;  
Best Local Similarity 100.0%; Pred. No. 5.4e-198;  
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MERRHPVCSCTGCTQPTQRCNSGCCIDSLFECDDTNCPCDASDEAAACEKYTSFGDELQRIH 60  
DB 308 MERRHPVCSCTGCTQPTQRCNSGCCIDSLFECDDTNCPCDASDEAAACEKYTSFGDELQRIH 367  
QY 61 FPSDKGHCVLDLPTDGLCKESIPRWYNNPFSEHCARFTYGGCYGNKNFEEQQCLSCRG 120  
DB 368 FPSDKGHCVLDLPTDGLCKESIPRWYNNPFSEHCARFTYGGCYGNKNFEEQQCLSCRG 427  
QY 121 ISKQDVFGLRREIPSTGSGVEMAVFLVICVWVAILGYCFFKNQKDFGHHHPP 180  
DB 428 ISKQDVFGLRREIPSTGSGVEMAVFLVICVWVAILGYCFFKNQKDFGHHHPP 487

QY 181 PTPASSTVSTTDETHLVYNNHTREL 206  
 DB 488 PTPASSTVSTTDETHLVYNNHTREL 513

RESULT 5  
 AAU92653

ID AAU92653 standard; protein; 513 AA.

XX AC AAU92653;

XX 30-APR-1999 (first entry)

XX Human HAI-1 protein.

XX Hepatocyte growth factor; HAI-1; HGF inhibiting factor; human; plasmin;

XX treatment; prevention; protease activity; plasma; urokinase; trypsin.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1-35

XX Protein /label= signal\_peptide

XX /label= HAI-1

XX JPI1035480-A.

XX 09-FEB-1999.

XX 15-JUL-1997; 97JP-00189480.

XX 15-JUL-1997; 97JP-00189480.

XX (MITU) MITSUBISHI CHEM CORP.

XX WPI; 1999-186215/16.

XX N-PSDB; AAX02200.

XX A preventive and/or treating agent for the diseases caused by the  
 PT exasperation of activity of protease - inhibits protease activity of  
 PT hepatocyte growth factor (HGF) activator.

XX Claim 7; Page 6-8; 8pp; Japanese.

XX This invention describes a preventive and/or treating agent for the  
 CC diseases caused by the exasperation of activity of protease of plasma  
 CC kallikrein, plasmin, urokinase and trypsin. The agent contains a protein,  
 CC HAI-1 which has the following properties, M.W. of ca. 40,000 to 57,000  
 CC Dalton by SDS-PAGE and an activity of inhibiting protease activity of  
 CC hepatocyte growth factor (HGF) activator. The HGF inhibiting activity of  
 CC the protein is specific. HAI-1 shows a high inhibiting activity on  
 CC plasmin, trypsin, HGF activator and plasma kallikrein but substantially  
 CC no inhibiting activity on thrombin. This sequence represents the human  
 CC HAI-1 protein

XX Sequence 513 AA;

Query Match 100.0%; Score 206; DB 2; Length 513;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-198;  
 Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCOPTQPCNSGCCIDSFLECDTPNCDFADSAEACEKTYSGFDELQRIH 60

DB 308 MERRHPVCSGTCOPTQPCNSGCCIDSFLECDTPNCDFADSAEACEKTYSGFDELQRIH 367

QY 61 FPSDKGHCVDLPDTGLCKESIPRWYINPFBSHCARFTYGGCYGNKNPFEEQQCLSCRG 120

DB 368 FPSDKGHCVDLPDTGLCKESIPRWYINPFBSHCARFTYGGCYGNKNPFEEQQCLSCRG 427

QY 121 ISKDVFGRLREIPITPSGSEMAVAVELVICIVVAILGVCFFKQKDFHGHHP 180

DB 428 ISKDVFGRLREIPITPSGSEMAVAVELVICIVVAILGVCFFKQKDFHGHHP 487

QY 181 PTPASSTVSTTDETHLVYNNHTREL 206  
 DB 488 PTPASSTVSTTDETHLVYNNHTREL 513

RESULT 6  
 ABU92043

ID ABU92043 standard; protein; 487 AA.

XX AC ABU92043;

XX 15-JUL-2003 (first entry)

XX Human protein modification and maintenance molecule-23 (PMMX-23).

XX Human; protein modification and maintenance molecule; PMM; cancer;  
 KW cell proliferation disorder; atherosclerosis; neurological disorder;  
 KW epilepsy; Huntington's disease; stroke; immune disorder; allergy;  
 KW inflammatory disorder; AIDS; developmental disorder; hypothyroidism;  
 KW Cushing's syndrome; gastrointestinal disorder; epithelial disorder;  
 KW infection; cytostatic; antiarteriosclerotic; anticonvulsant; nootropic;  
 KW neuroprotective; cerebroprotective; anti-HIV; anti-allergic; vulnary;  
 KW antiinflammatory; thyromimetic.

XX Homo sapiens.

XX WO2003031939-A2.

XX 17-APR-2003.

XX 11-OCT-2002; 2002WO-US032850.

XX 12-OCT-2001; 2001US-0329689P.

XX 25-OCT-2001; 2001US-0335703P.

XX 09-NOV-2001; 2001US-034887P.

XX 28-NOV-2001; 2001US-0334145P.

XX 06-DEC-2001; 2001US-0337451P.

XX 14-DEC-2001; 2001US-0340584P.

XX (INCY-) INCYTE GENOMICS INC.

XX Ramkumar J, Gorvad AE, Baughn MR, Emerling BM, Yang J, Lee SY;  
 PI Tran UK, Becha SD, Duggan BM, Lee EA, Griffin JA, Li JX;  
 PI Sprague WW, Hafalia AJA, Chawla NK, Lehr-Mason PM, Kable AE, Yue H;  
 PI Marquis JP, Yao MG, Richardson TW, Tang TY, Jin P, Chien D;  
 PI Bhatia U, Burrill JD, Lee S, Blake JJ, Ho A, Zheng W;

XX WPI; 2003-430274/40.

XX N-PSDB; ACA92438.

XX New human protein modification and maintenance molecules (PMM), useful  
 PT for diagnosing, treating and preventing diseases or conditions associated  
 PT with the aberrant PMM expression e.g. cancer, atherosclerosis, or  
 PT infections.

XX Claim 1; Page 263-264; 31pp; English.

XX The present invention relates to the isolation of human protein  
 CC modification and maintenance molecules (PMM), and the polynucleotide  
 CC sequences encoding them. A total of 40 PMM polypeptides (designated PMM  
 CC -1 to PMM-40) are disclosed. The sequences of the invention are useful  
 CC for diagnosing a condition or disease associated with the expression of  
 CC PMM in a subject, preparing a polyclonal or monoclonal antibody, and  
 CC generating an expression profile of a sample containing the  
 CC polynucleotides. The diseases or conditions associated with decreased  
 CC expression or overexpression of PMM are cell proliferation disorders  
 CC (e.g. cancer, atherosclerosis), neurological disorders (e.g. epilepsy,  
 CC Huntington's disease, stroke), immune/inflammatory disorders (e.g. AIDS,  
 CC allergies), developmental disorders (e.g. hypothyroidism, Cushing's  
 CC syndrome), gastrointestinal or epithelial disorders, and infections. The  
 CC PMM polypeptides or their fragments are useful in screening compounds  
 CC for effectiveness as agonists or antagonists of the polypeptides, or in

CC altering the expression of the target polynucleotide and compounds that  
CC specifically bind to, or modulate the activity of the polypeptide.  
CC ABU92021-ABU92060 represent the human PPMV polypeptides of the invention  
XX  
SQ Sequence 487 AA;

	Query Match	76.2%	Score 157;	DB 6;	Length 487;
	Best Local Similarity	100.0%;	Pred. No. 8.3e-149;		
	Matches 157;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	50	TSGFDELQRIHFPSDKGHCVLDPTGICKSGIIPRWYNPFSEHCARTYGGCYGNKNFE	109		
Db	331	TSGFDELQRIHFPSDKGHCVLDPTGICKSGIIPRWYNPFSEHCARTYGGCYGNKNFE	390		
Qy	110	EEQCLSECRGISKDVFGLRREIPIPTSGSVEAVAFVLICIVVWVAILGYCFFNQR	169		
Db	391	EEQCLSECRGISKDVFGLRREIPIPTSGSVEAVAFVLICIVVWVAILGYCFFNQR	450		
Qy	170	KDFGHGHHHPPTPASSTVSTTDETHLVNHTTRPL	206		
Db	451	KDFGHGHHHPPTPASSTVSTTDETHLVNHTTRPL	487		

RESULT 7  
AAB20113  
ID AAB20113 standard; protein: 529 AA.

XX AAB20113;  
AC  
XX  
DT 30-APR-20

AA  
DE Human immunostimulant PRO256.

XX PRO256; UNQ223; human; immune disease; autoimmune disease; antirheumatic;  
KW antiarthritic; antiinflammatory; antianemic; immunosuppressive;  
KW antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide;  
KW dermatologic; antipsoriatic; antiaesthetic; antiallergic;  
KW immunostimulant; protease-inhibitor.

OS Homo sapiens.

Key	Location/Qualifiers
Peptide	1..35
Modified-site	/label= Signal_peptide
Protein	29..35
Modified-site	/note= "N-myristoylation site"
Protein	36..529
Modified-site	/label= Mature_protein
Modified-site	43..49
Modified-site	/note= "N-myristoylation site"
Modified-site	66..70
Modified-site	/note= "Asn is N-glycosylated"
Modified-site	161..167
Peptide	/note= "N-myristoylation site"
Modified-site	193..196
Modified-site	/note= "cell attachment sequence"
Modified-site	212..218
Modified-site	/note= "N-myristoylation site"
Modified-site	235..239
Peptide	/note= "Asn is N-glycosylated"
Modified-site	257..300
Modified-site	/note= "pancreatic trypsin inhibitor (Kunitz) family protein motif"
Modified-site	281..287
Modified-site	/note= "N-myristoylation site"
Modified-site	282..288
Modified-site	/note= "N-myristoylation site"
Modified-site	285..291
Modified-site	/note= "N-myristoylation site"
Modified-site	310..316
Modified-site	/note= "N-myristoylation site"
Modified-site	313..319
Modified-site	/note= "N-myristoylation site"

FT	Peptide	347..356	
FT		/note= "low density lipoprotein class A domain protein	
FT		motif"	
FT	Peptide	398..441	
FT		/note= "pancreatic trypsin inhibitor (Kunitz) family	
FT		protein motif"	
FT	Modified-site	422..428	
FT		/note= "N-myristoylation site"	
FT	Modified-site	423..429	
FT		/note= "N-myristoylation site"	
FT	Modified-site	426..432	
FT		/note= "N-myristoylation site"	
FT	Domain	466..483	
FT		/note= "transmembrane domain"	
FT	Modified-site	523..527	
FT		/note= "Asn is N-glycosylated"	
XX			
PN	WC0200105972-A1.		

XX PD 25-JAN-2001.

15-MAR-2000: 2000WO-US006884.

XX  
PR 20-JUL-1999; 99US-0144758P.

XX  
PA (GETH ) GRNENTECH INC.

XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ;  
PI Gurney AL, Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D;  
PI Watanabe CK, Wood WI;  
XX WFI; 2001-103149/11.  
DR N-PSDB; AAF30055.  
DR

XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
PT diagnosing and treating immune-related disorders, such as multiple  
PT sclerosis, rheumatoid arthritis and diabetes.

xx  
PS  
Claim 20; Fig 12: 127pp; English.

The present sequence is that of novel human immunomodulator PRO256 (UNQ223), as deduced from cDNA (see AAF300355) isolated from a placental tissue library. PRO256 (58 kDa, pI 6.22) shows sequence homology to human bikunin protein, suggesting protease-inhibitor activity. The invention provides polynucleotides (see AAY30050-62) encoding novel human PRO proteins (see AAB20108-20) including PRO256. Claimed compositions comprising these proteins or their agonists are useful for increasing infiltration of inflammatory cells into a tissue of a mammal, stimulating or enhancing an immune response, or increasing the proliferation of T-lymphocytes in a mammal in response to an antigen. Claimed compositions comprising a PRO polypeptide or its antagonist have the opposite effect. A claimed method for treating an immune related disorder, such as a T cell disorder, involves administering a PRO polypeptide, an agonist antibody or an antagonist antibody. The disorder is selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathy, systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinated diseases (such as multiple sclerosis), autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis and Crohn's disease), gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated skin diseases (such as bullous skin disease, erythema multiforme and psoriasis), allergic diseases (such as asthma, allergic rhinitis, atopic dermatitis), food hypersensitivity and urticaria), immunologic diseases of the lung and transplantation associated diseases (such as graft rejection and graft-versus-host disease) (all claimed). Claimed methods of diagnosing these disorders comprise detecting the level of expression of the PRO gene. Also claimed are a method of identifying a compound capable of inhibiting the expression or activity of the PRO polypeptide, vectors, host cells, antibodies, and a method of stimulating the proliferation of T

```

CC lymphocytes using PRO256
XX Sequence 529 AA;
SQ

Query Match 70.4%; Score 145; DB 4; Length 529;
Best Local Similarity 100.0%; Pred. No. 1e-136;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCOPTQRCNSGCCIDSFLECDTNCPCDASDEAAACEKYTSGFDELQRIH 60
   |||||
Db 324 MERRHPVCSGTCOPTQRCNSGCCIDSFLECDTNCPCDASDEAAACEKYTSGFDELQRIH 383
   |||||

QY 61 FPSDKGHCVDLPTGTCCKESIPRWYNNPFSHCARFTYGCYGNKNPNFEEOQCLESRCG 120
   |||||
Db 384 FPSDKGHCVDLPTGTCCKESIPRWYNNPFSHCARFTYGCYGNKNPNFEEOQCLESRCG 443
   |||||

QY 121 ISKKDVGFLRRRPIPISTGSVEMAV 145
   |||||
Db 444 ISKKDVGFLRRRPIPISTGSVEMAV 468
   |||||

RESULT 8
AAE09332
ID AAE09332 standard; protein; 529 AA.
XX
AC AAE09332;
XX
DT 19-NOV-2001 (first entry)
XX
DE Human PRO256 protein.
XX
KW Human; PRO256 protein; cardiovascular; endothelial; angiogenic disorder;
KW cardiac hypertrophy; trauma; cardiac; age-related macular degeneration;
KW gene therapy; angiogenesis; protease activity; hepatocyte growth factor;
KW peripheral vascular disease; hepatic; renal injury; nephrotropic; tumour;
KW restinosis; tranquilizer; vulnery; cytostatic; hepatotropic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Peptide 1..35
FH /label= Signal_peptide
FT Modified-site 29..35
FT Protein 36..529
FT /note= "N-myristoylation site"
FT /note= "Human mature hepatocyte growth factor activator
FT inhibitor_PRO256"
FT Modified-site 43..49
FT /note= "N-myristoylation site"
FT Modified-site 65..70
FT /note= "Asn is N-glycosylated"
FT Modified-site 161..167
FT /note= "N-myristoylation site"
FT Region 193..199
FT /note= "N-myristoylation site"
FT Modified-site 212..218
FT /note= "Cell attachment sequence"
FT Modified-site 235..239
FT /note= "N-myristoylation site"
FT Modified-site 278..298
FT /note= "Asn is N-glycosylated"
FT Region
FT Modified-site 281..287
FT /note= "Pancreatic trypsin inhibitor family signature"
FT Modified-site 282..288
FT /note= "N-myristoylation site"
FT Modified-site 285..291
FT /note= "N-myristoylation site"
FT Modified-site 310..316
FT /note= "N-myristoylation site"
FT Modified-site 313..319
FT /note= "N-myristoylation site"
FT Region 419..438
FT /note= "Pancreatic trypsin inhibitor family signature"

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FT Modified-site 422..428
FT /note= "N-myristoylation site"
FT Modified-site 423..429
FT /note= "N-myristoylation site"
FT Modified-site 426..432
FT /note= "N-myristoylation site"
FT Domain 466..483
FT /label= Transmembrane_domain
FT Modified-site 523..527
FT /note= "Asn is N-glycosylated"
XX
FN WO200159100-A2.
XX
PD 16-AUG-2001.
XX
PP 19-DEC-2000; 2000WO-US034756.
XX
PR 11-FEB-2000; 2000WO-US003565.
PR 15-MAR-2000; 2000WO-US006884.
PR 28-NOV-2000; 2000US-0253665P.
XX
PA (GETH ) GENENTECH INC.
XX
XX Gurney AL, Kirchhofer DK, Wood WT;
XX
DR WPI; 2001-541567/60.
DR N-PSDB; AAD16721.
XX
FT An isolated polypeptide designated PRO256 useful for treating a
FT cardiovascular, endothelial, or angiogenic disorder.
XX
PS Claim 47; Fig 2; 124pp; English.
XX
CC The present invention relates to PRO256 or its agonist/antagonist may be
CC used to treat a cardiovascular, endothelial, or angiogenic disorder in a
CC mammal, especially a human with cardiac hypertrophy, trauma, a type of
CC tumour or age-related macular degeneration. PRO256 may be administered
CC together with a cardiovascular, endothelial, or angiogenic agent, a
CC chemotherapeutic agent, a growth inhibitory agent, or a cytotoxic agent.
CC PRO256 may also be used to treat the disorders above, preferably through
CC administration via ex vivo gene therapy. PRO256 or its agonist may be
CC used to inhibit endothelial cell growth, angiogenesis or protease
CC activity of a hepatocyte growth factor, whereas an antagonist of PRO256
CC may be used to stimulate endothelial cell growth, angiogenesis or
CC protease activity of a hepatocyte growth factor. Stimulation or
CC inhibition of the protease activity of a hepatocyte growth factor is
CC preferably carried out where a mammal has a cardiovascular, endothelial,
CC or angiogenic disorder selected from peripheral vascular disease, hepatic
CC or renal injury or a restinosis disorder. The present sequence is human
CC hepatocyte growth factor activator inhibitor, PRO256
XX
SQ Sequence 529 AA;

```

```

Query Match 70.4%; Score 145; DB 4; Length 529;
Best Local Similarity 100.0%; Pred. No. 1e-136;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCOPTQRCNSGCCIDSFLECDTNCPCDASDEAAACEKYTSGFDELQRIH 60
   |||||
Db 324 MERRHPVCSGTCOPTQRCNSGCCIDSFLECDTNCPCDASDEAAACEKYTSGFDELQRIH 383
   |||||

QY 61 FPSDKGHCVDLPTGTCCKESIPRWYNNPFSHCARFTYGCYGNKNPNFEEOQCLESRCG 120
   |||||
Db 384 FPSDKGHCVDLPTGTCCKESIPRWYNNPFSHCARFTYGCYGNKNPNFEEOQCLESRCG 443
   |||||

QY 121 ISKKDVGFLRRRPIPISTGSVEMAV 145
   |||||
Db 444 ISKKDVGFLRRRPIPISTGSVEMAV 468
   |||||

RESULT 9
AAU86133
ID AAU86133 standard; protein; 529 AA.

```

XX AC AAU86133;  
XX DT 15-JUL-2002 (first entry)  
XX DE Human PRO256 polypeptide.  
XX DE Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;  
KW leukemia; neuronal disorder; stromal disorder; blastocoele disorder;  
KW inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;  
KW neuroprotective.  
XX OS Homo sapiens.  
XX PN WC200153486-A1.  
XX PD 26-JUL-2001.  
XX PF 11-FEB-2000; 2000WO-US003565.  
XX PR 08-MAR-1999; 99WO-US005028.  
XX PR 11-MAR-1999; 99US-0123972P.  
XX PR 11-MAY-1999; 99US-0133459P.  
XX PR 02-JUN-1999; 99WO-US012252.  
XX PR 22-JUN-1999; 99US-0140650P.  
XX PR 22-JUN-1999; 99US-0140653P.  
XX PR 26-JUL-1999; 99US-0144758P.  
XX PR 26-JUL-1999; 99US-0145698P.  
XX PR 28-JUL-1999; 99US-0146222P.  
XX PR 17-AUG-1999; 99US-0149395P.  
XX PR 31-AUG-1999; 99US-0151889P.  
XX PR 01-SEP-1999; 99WO-US020111.  
XX PR 15-SEP-1999; 99WO-US021090.  
XX PR 30-NOV-1999; 99WO-US028313.  
XX PR 01-DEC-1999; 99WO-US028301.  
XX PR 01-DEC-1999; 99WO-US028634.  
XX PR 05-JAN-2000; 2000WO-US000219.  
XX PA (GETH ) GENENTECH INC.  
XX PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;  
PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;  
PI Watanabe CK, Wood WI;  
XX WPI; 2002-205567/26.  
XX DR N-PSDB; ABK40259.  
XX PT Thirty five nucleic acids encoding PRO polypeptides, useful for treating  
XX PT benign or malignant tumors, leukemias and lymphoid malignancies,  
XX PT inflammatory, angiogenic and immunologic disorders.  
XX PS Claim 61; Fig 12, 302pp; English.  
XX CC The present invention relates to the isolation of novel human PRO  
XX CC polypeptides and the polynucleotide sequences encoding them. The PRO  
XX CC polypeptides, agonists, antagonists or anti-PRO antibodies are useful for  
XX CC treating benign or malignant tumours (e.g. renal, kidney, bladder,  
XX CC breast, etc), leukemias and lymphoid malignancies, other disorders such  
XX CC as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,  
XX CC stromal and blastocoele disorders, inflammatory, immune and angiogenic  
XX CC disorders. The polynucleotide sequences are also useful in gene therapy.  
XX CC AAU86128-AAU86162 represent the human PRO polypeptides of the invention  
XX SQ Sequence 529 AA;  
Query Match 70.4%; Score 145; DB 5; Length 529;  
Best Local Similarity 100.0%; Pred. No. 1e-136;  
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MERRHPVCSGTCQPTQFCNSGCCIDSFLECCDTPNCPDASDEACEKYSGFDLQRIH 60  
DB 324 MERRHPVCSGTCQPTQFCNSGCCIDSFLECCDTPNCPDASDEACEKYSGFDLQRIH 383

QY 61 FPSDKGHCVDLPDTGLCKESIPRWYINPFSHCARFTYGGCYGNKNPFEEQCLSCRG 120  
DB 384 FPSDKGHCVDLPDTGLCKESIPRWYINPFSHCARFTYGGCYGNKNPFEEQCLSCRG 443  
QY 121 ISKDVFGRLREIPIPISTGSEMAV 145  
DB 444 ISKDVFGRLREIPIPISTGSEMAV 468  
RESULT 10  
ABB84837  
ID ABB84837 standard; protein; 529 AA.  
AC ABB84837;  
XX DT 16-MAY-2002 (first entry)  
XX DE Human PRO256 protein sequence SEQ ID NO:42.  
XX KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
KW age-related macular degeneration; arterial restenosis; angina;  
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
XX wound healing; chromosome mapping; gene mapping.  
XX OS Homo sapiens.  
XX PN WC200200690-A2.  
XX PD 03-JAN-2002.  
XX PF 20-JUN-2001; 2001WO-US019692.  
XX PR 23-JUN-2000; 2000US-0213637P.  
XX PR 20-JUL-2000; 2000US-0219556P.  
XX PR 25-JUL-2000; 2000US-0220624P.  
XX PR 25-JUL-2000; 2000US-0220664P.  
XX PR 28-JUL-2000; 2000WO-US020710.  
XX PR 02-AUG-2000; 2000US-0226959P.  
XX PR 17-AUG-2000; 2000US-00643657.  
XX PR 23-AUG-2000; 2000WO-US023522.  
XX PR 24-AUG-2000; 2000WO-US023328.  
XX PR 07-SEP-2000; 2000US-0230978P.  
XX PR 18-SEP-2000; 2000US-00664610.  
XX PR 18-SEP-2000; 2000US-00665350.  
XX PR 24-OCT-2000; 2000US-0242922P.  
XX PR 08-NOV-2000; 2000US-00709238.  
XX PR 08-NOV-2000; 2000WO-US030952.  
XX PR 10-NOV-2000; 2000WO-US030873.  
XX PR 20-DEC-2000; 2000US-00747259.  
XX PR 20-DEC-2000; 2000WO-US034956.  
XX PR 22-JAN-2001; 2001US-00767609.  
XX PR 28-FEB-2001; 2001US-00796498.  
XX PR 28-FEB-2001; 2001WO-US004520.  
XX PR 01-MAR-2001; 2001US-00806666.  
XX PR 03-MAR-2001; 2001US-00802706.  
XX PR 14-MAR-2001; 2001US-00808689.  
XX PR 22-MAR-2001; 2001US-00815744.  
XX PR 05-APR-2001; 2001US-00828366.  
XX PR 10-MAY-2001; 2001US-00854208.  
XX PR 10-MAY-2001; 2001US-00854280.  
XX PR 25-MAY-2001; 2001US-00866028.  
XX PR 25-MAY-2001; 2001US-00866034.  
XX PR 25-MAY-2001; 2001WO-US017092.  
XX PR 30-MAY-2001; 2001US-00870574.  
XX PR 01-JUN-2001; 2001WO-US017443.  
XX PR 01-JUN-2001; 2001WO-US017800.  
XX PA (GETH ) GENENTECH INC.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Masters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,  
 XX WPI; 2002-090516/12.  
 DR N-PSDB; ABL88092.  
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal.  
 XX Claim 11; Fig 42; 565pp; English.  
 XX ABL88072 to ABL88258 encode the PRO proteins given in ABL884817 to  
 CC ABL885003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.  
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The PRO polynucleotides have applications in molecular biology,  
 CC including use as hybridisation probes, and in chromosome and gene  
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the  
 CC exemplification of the present invention  
 XX Sequence 529 AA;

Query Match 70.4%; Score 145; DB 5; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 1e-136;  
 Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MERRHPVCSGTCPTOFRCSNGCCIDSFLECDTNCPCDASDAACEKVTSGFDELQRIH 60  
 Db 324 MERRHPVCSGTCPTOFRCSNGCCIDSFLECDTNCPCDASDAACEKVTSGFDELQRIH 383  
 QY 61 FPSDKGHCVLDPTGLCKESIPRWYNNPFSHCARFTYGGCYGNKNFEEQQCLSCRG 120  
 Db 384 FPSDKGHCVLDPTGLCKESIPRWYNNPFSHCARFTYGGCYGNKNFEEQQCLSCRG 443  
 QY 121 ISKDVFGRLRRRIPISTGSVEMAV 145  
 Db 444 ISKDVFGRLRRRIPISTGSVEMAV 468

RESULT 11  
 ID ABG34034  
 AC ABG34034  
 AC ABG34034;  
 DT 15-JUL-2002 (first entry)  
 XX Human Pro peptide #5.  
 DE Human; PRO; secreted protein; transmembrane protein; genetic disorder;  
 XX tumour; cancer.  
 KW Homo sapiens.  
 XX OS  
 OS W0200224888-A2.  
 XX 28-MAR-2002.  
 XX 29-AUG-2001; 2001WO-US027099.  
 XX 01-SEP-2000; 2000US-0229896P.  
 XX 05-SEP-2000; 2000US-0230821P.  
 XX 22-SEP-2000; 2000US-0235147P.  
 XX 10-NOV-2000; 2000WO-US030873.

PR 12-JAN-2001; 2001US-0261878P.  
 PR 16-JAN-2001; 2001US-0261910P.  
 PR 16-JAN-2001; 2001US-0261939P.  
 PR 16-JAN-2001; 2001US-0262150P.  
 PR 25-JAN-2001; 2001US-0264395P.  
 PR 02-FEB-2001; 2001US-0266421P.  
 PR 09-FEB-2001; 2001US-0267623P.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 09-MAR-2001; 2001US-0274399P.  
 PR 03-APR-2001; 2001US-0280982P.  
 PR 04-APR-2001; 2001US-0282129P.  
 PR 09-MAY-2001; 2001US-0282199P.  
 PR 25-MAY-2001; 2001WO-US017092.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 XX (GETH ) GENENTECH INC.  
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
 PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;  
 PI Fong S;  
 XX WPI; 2002-362426/39.  
 DR N-PSDB; ABK69965.  
 XX New PRO polypeptides and polynucleotides encoding the polypeptides,  
 PT useful in gene therapy, chromosome identification, tissue typing, or for  
 PT genetic analysis of individuals with genetic disorders.  
 XX Claim 11; Fig 10; 218pp; English.  
 XX This invention relates to the cDNA and protein sequences of novel  
 CC secreted and transmembrane polypeptides PRO polypeptides. The invention  
 CC also comprises a method for producing the proteins of the invention by  
 CC recombinant means and antibodies specific for the protein of the  
 CC invention. The antibody may be used for detecting the PRO proteins of the  
 CC invention and may be used to modify their activity. Polynucleotides may  
 CC be used as hybridisation probes for a cDNA library to isolate the full-  
 CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation  
 CC probes for mapping the gene which encodes that PRO and for genetic  
 CC analysis of individuals with genetic disorders, in assays to identify  
 CC other proteins or molecules involved in binding reaction, to generate  
 CC transgenic animals or knock-out animals which in turn are useful in the  
 CC development and screening of therapeutically useful reagents, for  
 CC chromosome identification, and tissue typing. The PRO polypeptides are  
 CC useful in gene therapy, and as molecular weight markers for protein  
 CC electrophoresis purposes. The sequences may also be used to detect  
 CC overexpression on PRO polypeptides in cancerous tumours and for screening  
 CC for differentially expressed genes using microarray technology. The  
 CC present sequence represents a human PRO protein of the invention  
 XX Sequence 529 AA;

Query Match 70.4%; Score 145; DB 5; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 1e-136;  
 Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MERRHPVCSGTCPTOFRCSNGCCIDSFLECDTNCPCDASDAACEKVTSGFDELQRIH 60  
 Db 324 MERRHPVCSGTCPTOFRCSNGCCIDSFLECDTNCPCDASDAACEKVTSGFDELQRIH 383  
 QY 61 FPSDKGHCVLDPTGLCKESIPRWYNNPFSHCARFTYGGCYGNKNFEEQQCLSCRG 120  
 Db 384 FPSDKGHCVLDPTGLCKESIPRWYNNPFSHCARFTYGGCYGNKNFEEQQCLSCRG 443  
 QY 121 ISKDVFGRLRRRIPISTGSVEMAV 145  
 Db 444 ISKDVFGRLRRRIPISTGSVEMAV 468



RESULT 12  
ID ABB95443 standard; protein; 529 AA.  
AC ABB95443;  
DT 19-JUL-2002 (first entry)  
XX Human angiogenesis related protein PRO256 SEQ ID NO: 42.  
DE  
DE Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KW cardiac; cytostatic; antiangiogenic; hypotensive; vulnary;  
KW antiarteriosclerotic.  
XX  
OS Homo sapiens.  
XX WO200208284-A2.  
PN  
PN 31-JAN-2002.  
PD  
XX 09-JUL-2001; 2001WO-US021735.  
XX 20-JUL-2000; 2000US-0219556P.  
PR 25-JUL-2000; 2000US-0220624P.  
PR 25-JUL-2000; 2000US-0220664P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 02-AUG-2000; 2000US-0222952P.  
PR 17-AUG-2000; 2000US-00643657.  
PR 23-AUG-2000; 2000WO-US023328.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 07-SEP-2000; 2000US-0230978P.  
PR 18-SEP-2000; 2000US-00664610.  
PR 18-SEP-2000; 2000US-00665350.  
PR 24-OCT-2000; 2000US-0242222P.  
PR 08-NOV-2000; 2000US-00708238.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 22-JAN-2001; 2001US-00767609.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006566.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00815744.  
PR 03-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 30-MAY-2001; 2001US-00870574.  
PR 30-MAY-2001; 2001WO-US017443.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
XX (GETH ) GENENTECH INC.  
PA (BAKE ) BAKER K P.  
PA (FERB ) FERRARA N.  
PA (GERB ) GERBER H.  
PA (GERR ) GERRITSEN M E.  
PA (GODD ) GODDARD A.  
PA (GODO ) GODOWSKI P J.  
PA (GURN ) GURNEY A L.  
PA (HILL ) HILLAN K J.  
PA (MARS ) MARSTERS S A.  
PA (PANJ ) PAN J.  
PA (PAON ) PAONI N F.  
PA (STEP ) STEPHAN J F.  
PA (WATA ) WATANABE C K.

(WILL ) WILLIAMS P M.  
(WOOD ) WOOD W I.  
PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX  
XX WPI; 2002-171999/22.  
DR N-PSDB; ABL95581.  
XX  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal.  
XX  
XX Claim 11; Fig 42; 567pp; English.  
XX  
XX The present invention provides the protein and coding sequences of human  
CC proteins. These are useful for treating or diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
CC hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The present sequence is a PRO protein of the invention  
XX  
XX Sequence 529 AA;  
SQ  
Query Match 70.4%; Score 145; DB 5; Length 529;  
Best Local Similarity 100.0%; Pred. No. 1e-136;  
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MERRHPCVSGTCQPTQFCNSGCCIDSFLECDTPNCPDASDEACCKYTSGFDELQRIH 60  
DB 324 MERRHPCVSGTCQPTQFCNSGCCIDSFLECDTPNCPDASDEACCKYTSGFDELQRIH 383  
QY 61 FPSDKGHCVLDPTGLCKESIPRYNYPNPFSEHCARFTYGGCYGNKNPFEEBOQCLESERG 120  
DB 384 FPSDKGHCVLDPTGLCKESIPRYNYPNPFSEHCARFTYGGCYGNKNPFEEBOQCLESERG 443  
QY 121 ISKDVFGRLRRRPIPTSGSVMAY 145  
DB 444 ISKDVFGRLRRRPIPTSGSVMAY 468  
RESULT 13  
ADA01278  
ID ADA01278 standard; protein; 529 AA.  
XX  
XX ADA01278;  
DT 06-NOV-2003 (first entry)  
XX  
XX Human PRO polypeptide #5.  
XX Human; PRO; secreted polypeptide; transmembrane polypeptide;  
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;  
KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;  
KW microvascular endothelial cell; endothelial cell tube formation;  
KW sports-related joint problem; articular cartilage defect; osteoarthritis;  
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.  
XX  
XX Homo sapiens.  
OS  
XX US2003068779-A1.  
XX  
XX 10-APR-2003.  
XX  
XX 16-SEP-2002; 2002US-00245107.  
XX  
XX 09-MAY-2001; 2001US-0290589P.  
PR 29-AUG-2001; 2001WO-US027099.  
PR 18-JUL-2002; 2002US-00197942.  
XX

PA (GETH ) GENENTECH INC.  
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
 PI Fong S;  
 XX WPI: 2003-625484/59.  
 DR N-PSDB; ADA01277.  
 XX  
 XX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for  
 PT stimulating proliferation of human microvascular endothelial cells, and  
 PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte  
 PT cells.  
 XX  
 XX Claim 11; Fig 10; 307pp; English.  
 XX  
 XX The invention relates to isolated human PRO polypeptides (secreted and  
 CC transmembrane polypeptides) and the polynucleotides encoding them. The  
 CC invention also relates to an antibody which specifically binds to a PRO  
 CC polypeptide, a method for stimulating the release of tumour necrosis  
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the  
 CC proliferation or differentiation of chondrocyte cells and a method for  
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,  
 CC colon, breast, prostate, rectal, cervical and liver tumours). The  
 CC polynucleotides are useful in molecular biology, including uses as  
 CC hybridisation probes, in chromosome and gene mapping, in generating  
 CC antisense RNA and DNA and in gene therapy. The polynucleotides may also  
 CC be used in preparing PRO polypeptides by recombinant techniques and in  
 CC generating either transgenic animals or knock-out animals which are  
 CC useful in the development and screening of therapeutically useful  
 CC reagents. The PRO polypeptides or antibodies are used in preparing a  
 CC medicament for treating a condition responsive to the polypeptides or  
 CC antibodies, such as tumours, for stimulating and inhibiting proliferation  
 CC of human microvascular endothelial cells, for inducing endothelial cell  
 CC tube formation and for treating sports-related joint problems, articular  
 CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence  
 CC represents a human PRO polypeptide of the invention.  
 XX  
 XX Sequence 529 AA;  
 XX  
 XX Query Match 70.4%; Score 145; DB 6; Length 529;  
 XX Best Local Similarity 100.0%; Pred. No. 1e-136;  
 XX Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MERRHPVCSGTCTQPTQFRCSNGCCIDSFLECDTNCPCDASDEAAACEKYSFGDELQRIH 60  
 DB 324 MERRHPVCSGTCTQPTQFRCSNGCCIDSFLECDTNCPCDASDEAAACEKYSFGDELQRIH 383  
 QY 61 FPSDKGHCVLDLPTGLCKESIPRWYNNPSEHCARTYGGCYGNKNPFEEOQCLESRCG 120  
 DB 384 FPSDKGHCVLDLPTGLCKESIPRWYNNPSEHCARTYGGCYGNKNPFEEOQCLESRCG 443  
 QY 121 ISKKDVFGLRRRPIPTSGSEMAV 145  
 DB 444 ISKKDVFGLRRRPIPTSGSEMAV 468  
 RESULT 14  
 ID ADA43707  
 XX ADA43707 standard; protein; 529 AA.  
 XX  
 XX ADA43707;  
 XX  
 XX 20-NOV-2003 (first entry)  
 XX  
 XX Human secreted/transmembrane polypeptide PRO256.  
 XX  
 XX Human; PRO; secreted protein; transmembrane protein;  
 KW endothelial cell tube formation; chondrocyte cell differentiation;  
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;  
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;  
 KW liver tumour; cytostatic; vaccine.  
 XX

Homo sapiens.

US2003064474-A1.

03-APR-2003.

16-SEP-2002; 2002US-00245859.

29-AUG-2001; 2001WO-US027099.

19-JUL-2002; 2002US-00197942.

(GETH ) GENENTECH INC.

Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
 Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
 Fong S;

WPI: 2003-605867/57.

N-PSDB; ADA43706.

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or  
 PRO21383, useful in molecular biology, chromosome and gene mapping, in  
 generating antisense RNA and DNA, and in gene therapy.

Claim 11; Fig 10; 308pp; English.

The invention relates to an isolated secreted/transmembrane (PRO)  
 polypeptide, having at least 80% sequence identity to a sequence selected  
 from any one of the 57 amino acid sequences given in specification, or to  
 a sequence encoded by a nucleic acid molecule selected from any one of  
 the nucleic acids deposited under any of the ATCC accession numbers given  
 in specification, or a sequence having at least 80% identity to PRO  
 lacking its associated signal peptide, an extracellular domain of PRO  
 with or without its associated signal peptide. Also included are vectors,  
 transformed host cells, anti-PRO antibodies, the nucleic acids encoding  
 PRO, PRO fusion proteins, inducing endothelial cell tube formation (by  
 administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,  
 PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and  
 an oligonucleotide probe derived from any one of the above nucleotide  
 sequences. PRO6018 polypeptide is useful for stimulating the  
 proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080  
 and PRO21383 polypeptides are useful for stimulating the proliferation of  
 human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006  
 polypeptides are useful for inhibiting the proliferation of human  
 microvascular endothelial cells. PRO polypeptides are useful for  
 detecting the presence of tumour in a mammal, including tumours of lung,  
 colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,  
 PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and  
 PRO34274 polypeptides are useful for inducing endothelial cell tube  
 formation. PRO or the antibody are useful in the preparation of a  
 medicament for treating a condition responsive to PRO polypeptide. The  
 oligonucleotide probes are useful for isolating genomic and cDNA  
 nucleotide sequences, for measuring or detecting the expression of an  
 associated gene, and as antisense probes. PRO nucleic acid is useful as a  
 hybridisation probe, in chromosome and gene mapping, in the generation of  
 antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and  
 PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The  
 present sequence represents a PRO protein.

Sequence 529 AA;

Query Match 70.4%; Score 145; DB 6; Length 529;

Best Local Similarity 100.0%; Pred. No. 1e-136;

Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCTQPTQFRCSNGCCIDSFLECDTNCPCDASDEAAACEKYSFGDELQRIH 60

DB 324 MERRHPVCSGTCTQPTQFRCSNGCCIDSFLECDTNCPCDASDEAAACEKYSFGDELQRIH 383

QY 61 FPSDKGHCVLDLPTGLCKESIPRWYNNPSEHCARTYGGCYGNKNPFEEOQCLESRCG 120

DB 384 FPSDKGHCVLDLPTGLCKESIPRWYNNPSEHCARTYGGCYGNKNPFEEOQCLESRCG 443

CC oligonucleotide probes are useful for isolating genomic and cDNA  
CC nucleotide sequences, for measuring or detecting the expression of an  
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a  
CC hybridisation probe, in chromosome and gene mapping, in the generation of  
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and  
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The  
CC present sequence represents a PRO protein.  
XX  
SQ Sequence 529 AA;

Query Match 70.4%; Score 145; DB 6; Length 529;  
Best Local Similarity 100.0%; Pred. No. 1e-136;  
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MERRHPVCSGTQPTQFRCSNGCCIDSPLECDTNCPCDASDEACEKYTSGFDELQRIH 60  
Db 324 MERRHPVCSGTQPTQFRCSNGCCIDSPLECDTNCPCDASDEACEKYTSGFDELQRIH 383  
Qy 61 FPSDKGHCVDLPTDTGLCKESIPRWYNNPFSERHARFTYGGCYGNKNPFEEBOCLES CRG 120  
Db 384 FPSDKGHCVDLPTDTGLCKESIPRWYNNPFSERHARFTYGGCYGNKNPFEEBOCLES CRG 443  
Qy 121 ISKQVFGRLRRRPIPISTGSVEMAV 145  
Db 444 ISKQVFGRLRRRPIPISTGSVEMAV 468

Search completed: April 22, 2004, 10:23:38  
Job time : 72 secs

Qy 121 ISKQVFGRLRRRPIPISTGSVEMAV 145  
Db 444 ISKQVFGRLRRRPIPISTGSVEMAV 468

RESULT 15  
ADA43475  
ID ADA43475 standard; protein; 529 AA.  
AC ADA43475;  
XX  
XX 20-NOV-2003 (first entry)  
XX Human secreted/transmembrane polypeptide PRO256.  
XX Human; PRO; secreted protein; transmembrane protein;  
XX endothelial cell tube formation; chondrocyte cell differentiation;  
XX microvascular endothelial cell; tumour; lung tumour; colon tumour;  
XX breast tumour; prostate tumour; rectal tumour; kidney tumour;  
XX liver tumour; cytostatic; vaccine.  
XX Homo sapiens.  
XX US2003073196-A1.  
XX 17-APR-2003.  
XX 18-SEP-2002; 2002US-00246210.  
XX 04-APR-2001; 2001US-0282199P.  
XX 29-AUG-2001; 2001WO-US027099.  
XX 18-JUL-2002; 2002US-00197942.  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
XX Fong S;  
XX WPI; 2003-743814/70.  
XX N-PSDB; ADA43474.  
XX New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or  
XX PRO21383 useful for stimulating the proliferation or differentiation of  
XX chondrocyte cells and detecting the presence of a tumor in a mammal.  
XX Claim 11; Fig 10; 307pp; English.  
XX The invention relates to an isolated secreted/transmembrane (PRO)  
XX polypeptide, having at least 80% sequence identity to a sequence selected  
XX from any one of the 57 amino acid sequences given in specification, or to  
XX a sequence encoded by a nucleic acid molecule selected from any one of  
XX the nucleic acids deposited under any of the ATCC accession numbers given  
XX in specification, or a sequence having at least 80% identity to PRO  
XX lacking its associated signal peptide, an extracellular domain of PRO  
XX with or without its associated signal peptide. Also included are vectors,  
XX transformed host cells, anti-PRO antibodies, the nucleic acids encoding  
XX PRO, PRO fusion proteins, inducing endothelial cell tube formation (by  
XX administering PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6006,  
XX PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and  
XX an oligonucleotide probe derived from any one of the above nucleotide  
XX sequences. PRO6018 polypeptide is useful for stimulating the  
XX proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080  
XX and PRO21383 polypeptides are useful for stimulating the proliferation of  
XX human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006  
XX polypeptides are useful for inhibiting the proliferation of human  
XX microvascular endothelial cells. PRO polypeptides are useful for  
XX detecting the presence of tumour in a mammal, including tumours of lung,  
XX colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,  
XX PRO189, PRO499, PRO6308, PRO5000, PRO10275, PRO21207, PRO20933 and  
XX PRO34274 polypeptides are useful for inducing endothelial cell tube  
XX formation. PRO or the antibody are useful in the preparation of a  
XX medicament for treating a condition responsive to PRO polypeptide. The

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2004, 04:41:39 ; Search time 4177 Seconds  
(without alignments)  
10759.536 Million cell updates/sec

Title: US-09-935-390A-4  
Perfect score: 1505  
Sequence: 1 GAATTCGGCAGCAGGAGCAG.....AAAAAAGTCTCGGGCGGC 1505

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hcc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hcc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	1099.4	73.0	1201	13	BX334952
c 2	1009.8	67.1	1056	13	BX382616
c 3	961.2	63.9	1073	13	BX360438
c 4	961	63.9	1192	13	BX381856

c 5	953.2	63.3	1164	13	BX378542
c 6	952.6	63.3	1026	13	BX344105
c 7	938.8	62.4	1201	9	AL542118
c 8	935	62.1	974	13	BX340192
c 9	912	60.6	1201	13	BX360812
c 10	907	60.3	1200	13	BX336601
c 11	902	59.9	1138	13	BX338259
c 12	898.4	59.7	1068	13	BX335408
c 13	898.2	59.7	1201	13	BX336602
c 14	894.4	59.4	1201	9	AL579407
c 15	886.6	58.9	1201	9	AL573797
c 16	882.2	58.6	1148	13	BX360076
c 17	876.6	58.2	1137	13	BX359232
c 18	875.4	58.2	994	13	BX360989
c 19	868.4	57.7	1201	13	BX357835
c 20	864.4	57.4	1183	9	AL558524
c 21	864.2	57.4	1108	9	AL558523
c 22	861.8	57.3	1201	13	BX339611
c 23	858.6	57.0	941	9	AL568344
c 24	855.6	56.9	1201	13	BX385809
c 25	855	56.8	1201	13	BX336936
c 26	854.2	56.8	1201	13	BX382069
c 27	851.8	56.6	1201	13	BX399630
c 28	851.8	56.6	1201	13	BX399955
c 29	841	55.9	1081	13	BX339553
c 30	839.4	55.8	971	13	BX338182
c 31	832	55.3	1193	9	AL568876
c 32	825.4	54.8	888	13	BQ687222
c 33	825	54.8	1200	13	BX386012
c 34	825	54.8	1201	13	BX359692
c 35	824	54.8	1201	13	BX339564
c 36	822.4	54.6	1201	13	BX339949
c 37	819.2	54.4	1201	9	AL513561
c 38	815.2	54.2	1004	13	BX360990
c 39	812.2	54.0	1201	13	BX378957
c 40	810.5	53.9	1062	13	BX398328
c 41	803.8	53.4	962	13	BX399483
c 42	787.6	52.3	862	14	CA488310
c 43	785	52.2	899	14	CA489864
c 44	784.6	52.1	856	13	BX400601
c 45	782.6	52.0	811	12	BG679448

#### ALIGNMENTS

RESULT 1  
BX334952/c  
LOCUS BX334952 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
DEFINITION clone CS0DI009YC11 3-PRIME, mRNA sequence.  
ACCESSION BX334952  
VERSION BX334952.1 GI:30310380  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1201)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 131 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 7854.f For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgl-bin/cluster.cgi?seq=CS0DI009AB06NP1&cluster=7854.f. Contact :  
Feng Liang Email: fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI009AS06NP1.

FEATURES

Location/Qualifiers  
1..1201  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DI009YCI1"  
/tissue type="PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 73.0%; Score 1099.4; DB 13; Length 1201;  
Best Local Similarity 97.1%; Pred. No. 6.8e-176;  
Matches 1115; Conservative 12; Mismatches 20; Indels 1; Gaps 1;  
326  
1166  
327  
1106  
387  
1046  
447  
986  
507  
926  
567  
866  
627  
807  
687  
747  
747  
687  
807  
627  
867  
567  
927  
507  
987  
447  
1047

387  
1107  
327  
1167  
267  
1227  
207  
1287  
147  
1347  
87  
1407  
27

RESULT 2

BX382616/c  
LOCUS  
DEFINITION  
BX382616 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
clone CS0DI083YF21 3-PRIME, mRNA sequence.

ACCESSION  
BX382616

VERSION  
BX382616.1

KEYWORDS  
EST.

SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens

REFERENCE  
1 (bases 1 to 1056)

AUTHORS  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLES  
Full-length cDNA libraries and normalization

JOURNAL  
Unpublished (2001)

COMMENT  
Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7854.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI083CC11NP1&cluster=7854.f. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ invitrogen Corporation 1600

Paraday Avenue Genoscope sequence ID : CS0DI083CC11NP1.

FEATURES

source

1..1056

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DI083YF21"

/tissue type="PLACENTA COT 25-NORMALIZED"

/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo (dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 67.1%; Score 1009.8; DB 13; Length 1056;  
Best Local Similarity 98.0%; Pred. No. 9.5e-161;  
Matches 1035; Conservative 4; Mismatches 15; Indels 2; Gaps 2;

398 CTGACGAGAGCATCCGGCTGTTACTCAACCCCTTCAGCGAACACTCGCCCGCTT 457  
1056 CTGACGAGAGCATCCGGCTGTTACTCAACCCCTTCAGCGAACACTCGCCCGCTT 997  
458 TACCTATGCTGTTTGAAGCAACAACTTTGAGAGAGAGCAGTGCCTCGA 517  
996 TACCTATGCTGTTTGAAGCAACAACTTTGAGAGAGAGCAGTGCCTCGA 937  
518 GTCTTGTGCGGCAATCTCCAGAGAGATGTTTGGCTCAGCGGGAATCCCATTC 577  
936 GTCTTGTGCGGCAATCTCCAGAGAGATGTTTGGCTCAGCGGGAATCCCATTC 878  
578 CAGCACAGGCTCTGTGAGATGCTGTGCGAGTCTTCTGTCTCATCTGCTTGTG 637  
877 CAGCACAGGCTCTGTGAGATGCTGTGCGAGTCTTCTGTCTCATCTGCTTGTG 819  
638 GGTAGCAATCTGTGCTTCTTCAAGAACAGAGAAAGCACTTCCACGACACCA 697  
818 GGTAGCAATCTGTGCTTCTTCAAGAACAGAGAAAGCACTTCCACGACACCA 759  
698 CCACACCCACACCCCTGCGAGTCTTCAAGTCTTCACTACTCCAGGACACGAGCA 757  
758 CCACACCCACACCCCTGCGAGTCTTCAAGTCTTCACTACTCCAGGACACGAGCA 699  
758 CCTGTCTATTAACACACCCCTGCGAGTCTTCAAGTCTTCACTACTCCAGGACACGAGT 817  
698 CCTGTCTATTAACACACCCCTGCGAGTCTTCAAGTCTTCACTACTCCAGGACACGAGT 639  
818 GCGCTGTCTGCTTCTGCAAGGACAGAGGCTGCGTGGGAAACCTTTGGAACAGACT 877  
638 GCGCTGTCTGCTTCTGCAAGGACAGAGGCTGCGTGGGAAACCTTTGGAACAGACT 579  
878 CTTCCTGCTTCCAGGCGCCCTGTGCTCAGAGACAGAGGCTCCAGCCCTCTTGGAGA 937  
578 CTTCCTGCTTCCAGGCGCCCTGTGCTCAGAGACAGAGGCTCCAGCCCTCTTGGAGA 519  
938 AGTCTCAGTAACTCAGTCTGAGAGCTTCAAGGTTTGGAGGACAGAGAAACCT 997  
518 AGTCTCAGTAACTCAGTCTGAGAGCTTCAAGGTTTGGAGGACAGAGAAACCT 459  
998 TGGGCGAGAGTACAGACTAGATGAGCTTCCCTGCTATAGGAGTTTGGAGAGTGGAG 1057  
458 TGGGCGAGAGTACAGACTAGATGAGCTTCCCTGCTATAGGAGTTTGGAGAGTGGAG 399  
1058 TTTTGTTCCTGTTTCAAGCTGCTGCTCCTACCCATGCTGCTAGGAGAGAGTGG 1117  
398 TTTTGTTCCTGTTTCAAGCTGCTGCTCCTACCCATGCTGCTAGGAGAGAGTGG 339  
1118 GTGTGTGTCAGACCTGAGGCGCCCAACCTGCTCCTCCGAGCTCCTCTTCCATGCTGTG 1177  
338 GTGTGTGTCAGACCTGAGGCGCCCAACCTGCTCCTCCGAGCTCCTCTTCCATGCTGTG 279  
1178 CGCCAGGCTGGAGGAGGACTTCCCTGCTGTAGTTTGTGCTGTAAAGATTGCTTTT 1237  
278 CGCCAGGCTGGAGGAGGACTTCCCTGCTGTAGTTTGTGCTGTAAAGATTGCTTTT 219  
1238 GTTATTTAATGCTGTGCTGCTGAGAGAGGAGGAGGCTGTTTGGCTCTCTA 1297  
218 GTTATTTAATGCTGTGCTGCTGAGAGAGGAGGAGGCTGTTTGGCTCTCTG 159  
1298 TCCTCTCTCTTCCCTTCCCTTGAAGTGTGCTCTCTGCTTGTGATCAGCCCTGCTC 1357  
158 TCCTCTCTCTTCCCTTCCCTTGAAGTGTGCTCTCTGCTTGTGATCAGCCCTGCTC 99  
1358 TAGACGACGACAGAGCAGGAGGAGTCTGCTGCTTCCGAGGCTTCCAGCCCTGCTC 1417  
98 TAGACGACGACAGAGCAGGAGGAGTCTGCTGCTTCCGAGGCTTCCAGCCCTGCTC 39  
1418 TTCTCCACATCAGAGCCCGCCCTGCTGCTTCCGAGGCTTCCAGCCCTGCTC 1453  
38 TTCTCCACATCAGAGCCCGCCCTGCTGCTTCCGAGGCTTCCAGCCCTGCTC 3

RESULT 3  
LOCUS BX360438/c  
DEFINITION Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
ACCESSION BX360438  
VERSION BX360438.1  
KEYWORDS GI:30378436  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1073)  
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 7854.f For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DI070BA10NP1&cluster=7854.f. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ invitrogen Corporation 1600  
Paradise Avenue Genoscope sequence ID : CS0DI070BA10NP1.  
Location/Qualifiers  
1..1073  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DI070BA10"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/notes="1st strand cDNA was primed with a NotI-oligo (dm)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match 63.9%; Score 961.2; DB 13; Length 1073;  
Best Local Similarity 98.0%; Pred. No. 1.5e-152;  
Matches 1017; Conservative 8; Mismatches 7; Indels 6; Gaps 5;  
Qy 403 AGAGAGCATCCCGCTGCTACTACACCCCTTCAGCGAACACTCGCCCGCTTACCT 462  
Db 1032 AAGAGAGCATCCCGCTGCTACTACACCCCTTCAGCGAACACTCGCCCGCTTACCT 975  
Qy 463 ATGCTGTTTCTTACGGCAACAACTTTTCAAGAGAGAGAGTCTCGAGTCTT 522  
Db 974 ATGCTGTTTCTTACGGCAACAACTTTTCAAGAGAGAGAGTCTCGAGTCTT 916  
Qy 523 GTCCGCGCATCTCAAGAGAGTGTGTTTGGCTGAGGCGGGAATCCCATTCGAGCA 582  
Db 915 GTCCGCGCATCTCAAGAGAGTGTGTTTGGCTGAGGCGGGAATCCCATTCGAGCA 857  
Qy 583 CAGCTCTGTGAGAGTGTGTTTGGCTGAGTGTCTGCTGCTATCTGCTGCTGCTGCTG 642  
Db 856 CAGCTCTGTGAGAGTGTGTTTGGCTGAGTGTCTGCTGCTATCTGCTGCTGCTGCTG 797  
Qy 643 CCACTTGTGCTTACTGCTTCTTCAAGAACAGAGAGAGTCTTCCAGGACACCAACC 702  
Db 796 CCACTTGTGCTTACTGCTTCTTCAAGAACAGAGAGAGTCTTCCAGGACACCAACC 737  
Qy 703 ACCACACCAACCCCTGCGAGTCTTCACTGCTTCCACTACCGAGGACACCGAGCACCTGG 762  
Db 736 ACCACACCAACCCCTGCGAGTCTTCACTGCTTCCACTACCGAGGACACCGAGCACCTGG 677  
Qy 763 TCTATTAACCAACCAACCGCGGCCCTCTGAGCTTGGTCTTCACTGCTGCTTCACTGCTG 822  
Db 676 TCTATTAACCAACCAACCGCGGCCCTCTGAGCTTGGTCTTCACTGCTGCTTCACTGCTG 617









[illegible]

Db 853 CCCAGCACAGGCTCTGGAGATTGGTGTGCACTGTTCCTGGTCACTCTGCATTGGTG 794  
 QY 636 GTGGTAGCATCTTTGGGTTACTGTTCTTCAAGAACAGAGAAAGGACTTCCACGACAC 695  
 Db 793 GTGGTAGCATCTTTGGGTTACTGTTCTTCAAGAACAGAGAAAGGACTTCCACGACAC 734  
 QY 696 CACCACACACACACACACACCCCTGCGAGCTCCACTGTCTCCACTACCGAGGACACGGAG 755  
 Db 733 CACCACACACACACACACCCCTGCGAGCTCCACTGTCTCCACTACCGAGGACACGGAG 674  
 QY 756 CACTGTGTCTATAACACACACACCGCGCCCTCTGAGCCCTGGGTCTTACCGGCTCTCAC 815  
 Db 673 CACTGTGTCTATAACACACACACCGCGCCCTCTGAGCCCTGGGTCTTACCGGCTCTCAC 614  
 QY 816 TGGCCCTGTCTTCTGCTTGGCCAGCGAGAGCCCTGGGCTGCGAAACCTTTGAAACCA 875  
 Db 613 TGGCCCTGTCTTCTGCTTGGCCAGCGAGAGCCCTGGGCTGCGAAACCTTTGAAACCA 554  
 QY 876 CTCCTGTCTGTTTCCAGGCCCCACTGTGCTCAGAGACACAGGCTCCAGCCCTCTTGA 935  
 Db 553 CTCCTGTCTGTTTCCAGGCCCCACTGTGCTCAGAGACACAGGCTCCAGCCCTCTTGA 494  
 QY 936 GAAGTCTCAGCTAAGCTCAGCTCTGAGAAAGCTCAAGGTTTGGAGGACAGAAACC 995  
 Db 493 GAAGTCTCAGCTAAGCTCAGCTCTGAGAAAGCTCAAGGTTTGGAGGACAGAAACC 434  
 QY 996 CTTGGGCGAAGTACAGACTAGATGGA CTTGCTGCTGATAGAGTTTGAGGAAGTTGG 1055  
 Db 433 CTTGGGCGAAGTACAGACTAGATGGA CTTGCTGCTGATAGAGTTTGAGGAAGTTGG 374  
 QY 1056 AGTTTGTCTCTGTTTCAAGCTGCTGCTTACCCCTACCCCTGCTGCTAGAGAGGAGCT 1115  
 Db 373 AGTTTGTCTCTGTTTCAAGCTGCTGCTTACCCCTACCCCTGCTGCTAGAGAGGAGT 314  
 QY 1116 GGGTGTGTGTCAGACCTGTGAGGCCCCAA CCGTGTCTTCCGAGCTCTTCCATGCTG 1175  
 Db 313 GGGGCGGTGTGAGACCTGTGAGGCCCCAA CCGTGTCTTCCGAGCTCTTCCATGCTG 254  
 QY 1176 TGGCCCGAGGCTGGGAGGAGGACTTCCCTGTGTAGTTTGTCTGTAAGAGTTGCTTT 1235  
 Db 253 TGGCCCGAGGCTGGGAGGAGGACTTCCCTGTGTAGTTTGTCTGTAAGAGTTGCTTT 194  
 QY 1236 TTGTTTATTAATGCTGTGGCATGGGTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 1295  
 Db 193 TTGTTTATTAATGCTGTGGCATGGGTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 134  
 QY 1296 TATCT 1355  
 Db 133 TATCT 74  
 QY 1356 CTTAGACACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 1415  
 Db 73 CTTAGACACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 14  
 QY 1416 GGTTCCTCAACAT 1428  
 Db 13 GGTTCCTCAACAT 1

RESULT 9  
 BX360812/c  
 LOCUS  
 DEFINITION BX360812 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
 clone CS0D1075YN13 3-PRIME, mRNA sequence.  
 ACCESSION BX360812  
 VERSION BX360812.1 GI:30366459  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1201)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

# TITLE JOURNAL COMMENT

Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seque@genoscope.cns.fr; Web: www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 7854.f For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0D1075CG07NP1&cluster=7854.f. Contact :  
 Feng Liang Email: fliang@lifetech.com URL :  
 http://fulllengthch.invitrogen.com/ invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0D1075CG07NP1.

## FEATURES

### source

1. .1201  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0D1075YN13"  
 /tissue\_type="PLACENTA COT 25-NORMALIZED"  
 /clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 60.6%; Score 912; DB 13; Length 1201;  
 Best Local Similarity 97.18; Pred. No. 2 9e-144;  
 Matches 932; Conservative 5; Mismatches 22; Indels 1; Gaps 1;  
 QY 482 CAAGAACACTTTGAGAGAGAGCAGCAGTCCCTGAGTCTTGTGCGGGGATCTCCAGAA 541  
 Db 969 CAACAGANMACTTTGAGGAGRGCAAGTGCCTCGAGTCTTGTGCGGCATCTCCAGAA 910  
 QY 542 GGATGTGTTGGCTGAGCGGGGAAATCCCATTTCCAGACACAGGCTCTGTGAGATGC 601  
 Db 909 GGATGTGTTGSKCTGAGCGGGGAAATCCCATTTCCAGACACAGGCTCTGTGAGATGC 850  
 QY 602 TGTGCGAGTGTCTGTGTCATCTGCAATTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 661  
 Db 849 TGTGCGAGTGTCTGTGTCATCTGCAATTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 790  
 QY 662 CTTCAAGAACACAGAGAAAGGACTTCCAGGACACACACACACACACACACACACACAC 721  
 Db 789 CTTCAAGAACACAGAGAAAGGACTTCCAGGACACACACACACACACACACACACAC 730  
 QY 722 CAGTCCACTGTCTCCTACACGAGACACGAGACACCTGTCTATAACACACACAGG 781  
 Db 729 CAGTCCACTGTCTCCTACACGAGACACGAGACACCTGTCTATAACACACACAGG 670  
 QY 782 GCGCCCTCTGAGCCTGGGTCTCACCCTGTCTCAGCTGCGCCCTGCTTCTGTGCTCAAGGC 841  
 Db 669 GCGCCCTCTGAGCCTGGGTCTCACCCTGTCTCAGCTGCGCCCTGCTTCTGTGCTCAAGGC 610  
 QY 842 AGAGCCTGGGCTGGGAAACCTTTGGAACACGAGCTCTGCTGTGTTCCAGGCCACTG 901  
 Db 609 AGAGCCTGGGCTGGGAAACCTTTGGAACACGAGCTCTGCTGTGTTCCAGGCCACTG 550  
 QY 902 TGCTCTAGACACACAGGCTCCAGCCCTCTTGTGAGAGTCTCAGCTAAGCTCAGCTCTCTG 961  
 Db 549 TGCTCTAGACACACAGGCTCCAGCCCTCTTGTGAGAGTCTCAGCTAAGCTCAGCTCTCTG 490  
 QY 962 AGAAGCTCAAGGTTTGGAGGACAGAAACCTTTGGGCCAGAGTACGAGCTAGAT 1021  
 Db 489 AGAAGCTCAAGGTTTGGAGGACAGAAACCTTTGGGCCAGAGTACGAGCTAGAT 430  
 QY 1022 GGAACCTCCCTGCATAGGAGTTTGGAGAGAGTGTGGAGTTTGTCTCTGTCTCAAGCTG 1081  
 Db 429 GGAACCTCCCTGCATAGGAGTTTGGAGAGAGTGTGGAGTTTGTCTCTGTCTCAAGCTG 370  
 QY 1082 CTTGTCCCTACCCCTAGTGTCTAGGAGAGGAGTGGGGTGTGTCTCAGACCCCTGGAGGCC 1141





191 TGGGTGACGAGGAGGAGAGGCGCTGTTGGCGTSTCTATCTCTCTTCTCTTCCGCC 132

Db

1318 AAGATTGAGCTCTTGCCCTTGATCAGCCCAACCTGGCTGTAGACCAGACAGACAGCCA 1377

Qy

131 AAGATTGAGCTCTTGCTTTGATCAGCCCAACCTGGCTGTAGACCAGACAGACAGCCA 72

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1378 GGGAGACTCAGCTGATTCGAGGCCCAACCCCAAGTTCTCCAAATCATCAGCC 1435

Qy

71 GGGAGACTCA-STGATTCGAGGCCCAACCCCAAG-TTCCAAATCATCAGGCC 16

Db

## ORIGIN

RESULT 13				
EX336602	1201 bp	mrna	linear	EST 02-MAY-2003
LOCUS				
DEFINITION	EX336602 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0D1030YE23 5-PRIME, mrna sequence.			
ACCESSION	EX336602			
VERSION	EX336602.1	GI:30339518		
KEYWORDS	ZST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 131 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7854.f For more information about this cluster, see <a href="http://www.genoscope.cns.fr/http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0D1030AC120P1&amp;cluster=7854.f">http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CS0D1030AC120P1&amp;cluster=7854.f</a> . Contact : Feng Liang Email : <a href="mailto:fliang@lifetech.com">fliang@lifetech.com</a> URL : <a href="http://fulllength.invitrogen.com/Invitrogen">http://fulllength.invitrogen.com/Invitrogen</a> Corporation 1600 Paradise Avenue, Genoscope sequence ID : CS0D1030AC120P1.			

**FEATURES** source

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/notes="1st strand cDNA was primed with a NotI-oligo(3T) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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**ORIGIN**

	Query Match	59.7%;	Score 898.2;	DB 13;	Length 1201;
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	Matches 980;	Conservative	32;	Mismatches 60;	Indels 15; Gaps 5;
Qy	239	CTGCATCGACAGTTTCTCTGGAGTGTGACGACACCCCGACCTGCCGACGCTCCGACGA	298		
Db	61	CGGGATCGACAGTTTCTCTGGAGTGTGACGACACCCCGACCTGCCGACGCTCCGACGA	120		
Qy	299	GGCTGCCCTGTGAAAAATACACGAGTGCCTTTGACGAGTCCGAGCGCATTCATTTTCCCGAC	358		
Db	121	GGCTGCCCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGGGCATTCATTTTCCCGAC	180		
Qy	359	CGACAAAGGGGCACTCGCTGGAGACCTGCCAGACACACAGGACTCTGCGAAGGAGAGCATCCCGCG	418		
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Qy	419	CTGGTACTACAAACCCCTTCACGGAACACTGCGCCCGCTTTTACCTATGCTGGTGTGTGTAACGG	478		
Db	243	CTGGTACTACAAACCCCTTCACGGAACACTGCGCCCGCTTTTACCTATGCTGGTGTGTGTAACGG	300		

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 1201)  
Li, W.B., Gruber, C., Jessse, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 16, 2001 this sequence version replaced gi:12944423.

Contact: Genoscope  
Genoscope - Centre National de Séquençage  
BP 191 91006 EVRY cedex - France  
Email: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
7854.1 For more information about this cluster, see

Feng Liang Email : [liang@lifetech.com](mailto:liang@lifetech.com) URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0DH004C0A7NP1.  
 cgl-bin/cluster.cgi?seq=CS0DH004C0A7NP1&cluster=7854.f. Contact :  
<http://www.genoscope.cns.fr/>

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FEATURES
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                    with a NotI-oligo(dT) primer. Five prime end enriched,
                    double-strand cDNA was digested with Not I and cloned into
                    the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                    Library was not normalized."

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ORIGIN

Query Match	59.4%	Score 894.4	DB 9	Length 1201
Best Local Similarity	90.6%	Pred. No. 2.7e-141		
Matches 931	Conservative 45	Mismatches 48	Indels 4	Gaps 3

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Db		
479	CAACAAGAACACTTTTGAGGAGAGACGACGAGTGCCTCGAGTCTTGTCCGCGCATCTCAA	538
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911 GAGGATGTTGGCTGAGCGGGAAATCCCATTCCTGAGCACAGGCTCTGTGGAGAT 852  
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599 GGCCTGCGCAGTGTTCCTGGTCATCTGCAATTGTGGTGGTAGCCATCTGGGTTACTG 658

851 -GATTCGCAGAGTCTCTGGTCAATCGCATGTGTGTGTGTACCCATCTTGGGTTACTG 793 Db

659 CTCTTTCAAGAACCAGAAAGGAATTCCAAGGACACCAACCAACCAACCAACCCCC 718 QY

792 CTCTTTCAAGAACCAAGAAAGGATTTCACGGACACCAACCAACCAACCAACCCCC 733 Db

719	TGCCAGCTGCACCTGTCTCCACTACCGAGGACACGAGGACACCTGGTCTTATAACACACACAC	778
732	TGCCAGCTGCACCTGTCTCCACTACCGAGGACACGAGGACACCTGGTCTTATAACACACACAC	873
779	GCGGCCCCCTTCAGCCTGGGGTCTCACCGGCTCTCACCTGGGCCCTGGTCTCTGTTGGCAA	838

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552 CTGTGCTTCAGAGACGAGGGCTCCAGGCCCTCTTTGGAGAGAGTCTTCAGCTTAAGCTCACGMM 493

\_\_\_\_\_

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Contact: Genoscope  
Genoscope - Centre National de Séquençage  
BP 191 91006 EVRY cedex - France  
Email: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
7854.1 For more information about this cluster, see

Feng Liang Email : [liang@lifetech.com](mailto:liang@lifetech.com) URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0DH004C0A7NP1.  
 cgl-bin/cluster.cgi?seq=CS0DH004C0A7NP1&cluster=7854.f. Contact :  
<http://www.genoscope.cns.fr/>

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                /mol_type="mRNA"
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                    double-strand cDNA was digested with Not I and cloned into
                    the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                    Library was not normalized."

```

ORIGIN

Query Match	59.4%	Score 894.4	DB 9	Length 1201
Best Local Similarity	90.6%	Pred. No. 2.7e-141		
Matches 931	Conservative 45	Mismatches 48	Indels 4	Gaps 3

1029	CSSETGTACAAAGCCCTTMSGACACKCCCGCTTTCCTATGGTG--TTGTTATG	972
479	CAACAAGAACAACTTTTGAGGAGAGACGACGATGCTTCGAGCTCTTTCGCGGCATCTCAA	538
971	CACACAGAACAACTTTTGGAGAGACGACGATGCTTCGAGCTCTTTCGCGGCATCTCAA	912
479	CAACAAGAACAACTTTTGAGGAGAGACGACGATGCTTCGAGCTCTTTCGCGGCATCTCAA	538
971	CACACAGAACAACTTTTGGAGAGACGACGATGCTTCGAGCTCTTTCGCGGCATCTCAA	912

571 GAGGATGTTGGCTGAGCGGGAAATCCCATTCCTGAGCACAGGCTCTGTGGAGAT 598  
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539 GAGGATGTTGGCTGAGCGGGAAATCCCATTCCTGAGCACAGGCTCTGTGGAGAT 598  
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911 GAGGATGTTGGCTGAGCGGGAAATCCCATTCCTGAGCACAGGCTCTGTGGAGAT 852  
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599 GGCCTGCGCAGTGTTCCTGGTCATTCGATTTGTGGTGGTAGCCATTTGGGTTACTG 658

851 -GATTCGACAGATTCCTGGTCATTCGATGTGTGTGTGATGCCATCTTGGGTACTG 793 Db

659 CTCTTTCAAGAACACGAGAAAGGATTCCACGGACACCAACCAACCAACCAACCC 718 QY

792 CTCTTTCAAGAACACGAGAAAGGATTCCACGGACACCAACCAACCAACCAACCC 733 Db

719	TGCCAGCTGCACCTGTCTCCACTACCGAGGACACGAGGACACCTGGTCTTATAACACACACAC	778
732	TGCCAGCTGCACCTGTCTCCACTACCGAGGACACGAGGACACCTGGTCTTATAACACACACAC	873
779	GCGGCCCCCTTCAGCCTGGGGTCTCACCGGCTCTCACCTGGGCCCTGGTCTCTGTTGGCAA	838

db	672	CGGGCCCTCTGAGGCTGGGCTCACCGGCTCTACCTGGGCTTGCCTCTGCTGGCAA	613
Qy	839	GGCAGAGGCTCGGGCTGGGAAAACTTTGGAAACGAGACTCTTGCTCTTTCCAGGCCCA	898
db	612	GGCAGAGGCTCGGGCTGGGAAAACTTTGGAAACGAGACTCTTGCTCTTTCCAGGCCCA	553

899 CTGTGCTTCAGAGACCAGGGCTCCAGGCCCTCTTTGGAGAGCTCTTCAGCTTAAGGCTCAGGTC 958  
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QY 1259 GGGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1318
Db 192 GGGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 133
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## RESULT 15

AL573797/c

LOCUS

DEFINITION

AL573797 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

clone CS0D1055YC15 3-PRIME, mRNA sequence.

AL573797

VERSION

AL573797.2 GI:31295133

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS

TITLES

JOURNAL

COMMENT

On Feb 16, 2001 this sequence version replaced gi:12933393.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7854.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0D1055AB08NP1&amp;cluster=7854.f. Contact:

Feng Liang Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/Invitrogen Corporation 1600

Paradise Avenue Genoscope sequence ID: CS0D1055AB08NP1.

FEATURES

Location/Qualifiers

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/notes="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with NotI and cloned into the NotI and EcoRV

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Job time : 4182 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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Run on: April 22, 2004, 05:09:18 ; Search time 659 Seconds  
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Title: US-09-935-390A-4  
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Scoring table: IDENTITY\_NUC  
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Searched: 2307579 seqs, 2254313464 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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39	1468	97.5	2482	15	US-10-223-085-41	Sequence 41, Appli
40	1468	97.5	2482	15	US-10-237-636-9	Sequence 9, Appli
41	1468	97.5	2482	15	US-10-238-325-9	Sequence 9, Appli
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43	1468	97.5	2482	15	US-10-238-411-9	Sequence 9, Appli
44	1468	97.5	2482	15	US-10-243-124-9	Sequence 9, Appli
45	1468	97.5	2482	15	US-10-243-425-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-09-935-390A-4  
; Sequence 4, Application US/09935390A  
; Patent No. US20020076761A1  
; GENERAL INFORMATION:  
; APPLICANT: Escobedo, Jaime  
;           Garcia, Pablo  
;           Quianjin, Hu  
;           Williams, Lewis T.  
;           Kothakota, Srinivas  
; TITLE OF INVENTION: Secreted Human Proteins  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
;           ADDRESSEE: Chiron Corporation  
;           STREET: 4560 Horton Street  
;           CITY: Emeryville  
;           STATE: CA  
;           COUNTRY: USA  
;           ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/935,390A  
; FILING DATE: 22-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/988,671  
; FILING DATE: 1997-12-11  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jane E. R. Potter  
; REGISTRATION NUMBER: 33,332  
; REFERENCE/DOCKET NUMBER: 1369,002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 923-2718





Prior Filing Date:	2000-08-23
Prior Application Number:	PCT/US00/23328
Prior Filing Date:	2000-08-24
Prior Application Number:	US 60/230,978
Prior Filing Date:	2000-09-07
Prior Application Number:	US 60/000,000
Prior Filing Date:	2000-09-15
Prior Application Number:	US 09/664,610
Prior Filing Date:	2000-09-18
Prior Application Number:	US 09/665,350
Prior Filing Date:	2000-09-18
Prior Application Number:	US 60/242,922
Prior Filing Date:	2000-10-24
Prior Application Number:	US 09/709,238
Prior Filing Date:	2000-11-08
Prior Application Number:	PCT/US00/30952
Prior Filing Date:	2000-11-08
Prior Application Number:	PCT/US00/30873
Prior Filing Date:	2000-11-10
Prior Application Number:	PCT/US00/32678
Prior Filing Date:	2000-12-01
Prior Application Number:	US 09/747,259
Prior Filing Date:	2000-12-20
Prior Application Number:	PCT/US00/34956
Prior Filing Date:	2000-12-20
Prior Application Number:	US 09/767,609
Prior Filing Date:	2001-01-22
Prior Application Number:	US 09/796,498
Prior Filing Date:	2001-02-28
Prior Application Number:	PCT/US01/06520
Prior Filing Date:	2001-02-28
Prior Application Number:	PCT/US01/06666
Prior Filing Date:	2001-03-01
Prior Application Number:	US 09/802,706
Prior Filing Date:	2001-03-09
Prior Application Number:	US 09/808,689
Prior Filing Date:	2001-03-14
Prior Application Number:	US 09/816,744
Prior Filing Date:	2001-03-22
Prior Application Number:	US 09/828,366
Prior Filing Date:	2001-04-05
Prior Application Number:	US 09/854,208
Prior Filing Date:	2001-05-10
Prior Application Number:	US 09/854,280
Prior Filing Date:	2001-05-10
Prior Application Number:	US 09/866,028
Prior Filing Date:	2001-05-25
Prior Application Number:	US 09/866,034
Prior Filing Date:	2001-05-25
Prior Application Number:	PCT/US01/17092
Prior Filing Date:	2001-05-25
Prior Application Number:	US 09/870,574
Prior Filing Date:	2001-05-30
Prior Application Number:	PCT/US01/17443
Prior Filing Date:	2001-05-30
Prior Application Number:	PCT/US01/17800
Prior Filing Date:	2001-06-01
Prior Application Number:	PCT/US01/19692
Prior Filing Date:	2001-06-20
Prior Application Number:	PCT/US01/00000
Prior Filing Date:	2001-06-28
Number of Seq ID Nos:	383
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Length:	2482
Type:	DNA
Organism:	Homo sapiens
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Best Local Similarity	99.3%; Pred. No. 0;
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Best Local Similarity 99.3%; Pred. No. 0;  
Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;



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; Sequence 9, Application US/1024589
; Publication No. US2003006447A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P36301C78
; CURRENT APPLICATION NUMBER: US/10/245,859
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
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; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 9
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-859-9
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Best Local Similarity 99.3%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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Db 1295 GAAAAATACAGAGTGGCTTTGACAGCTCAGCGCATGCAATTTCCCGAGCGACAAGGG 1354
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; Sequence 9, Application US/10245103			
; Publication No. US2003068778A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin			
; APPLICANT: Baton, Dan			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Grimaldi, J. Christopher			
; APPLICANT: Gurney, Austin			
; APPLICANT: Smith, Victoria			
; APPLICANT: Stephan, Jean-Phillippe			
; APPLICANT: Watanabe, Colin			
; APPLICANT: Wood, William			
; APPLICANT: Zhang, Zemin			
; APPLICANT: Fong, Sherman			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; FILE OF INVENTION: ACIDS ENCODING THE SAME			
; FILE REFERENCE: P3630R1C112			
; CURRENT APPLICATION NUMBER: US/10/245,103			
; CURRENT FILING DATE: 2002-09-17			
; PRIOR APPLICATION NUMBER: 10/197942			
; PRIOR FILING DATE: 2002-07-18			
; PRIOR APPLICATION NUMBER: 60/059114			
; PRIOR FILING DATE: 1997-09-17			
; PRIOR APPLICATION NUMBER: 60/063046			



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RESULT 10

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; Sequence 9, Application US/10245143
; Publication No. US2003068780A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Pilvaroff, Ellen
; APPLICANT: Goddard, Audrey

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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P630R1C90
; CURRENT APPLICATION NUMBER: US/10/245,143
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
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; TYPE: DNA
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; US-10-245-143-9

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Query Match 97.5%; Score 1468; DB 15; Length 2482;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY 1029 CTGCTAGGAGTTTGGAGAGTGGAGTTTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1088  
DB 2015 CTGCTAGGAGTTTGGAGAGTGGAGTTTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2074  
QY 1089 CTACCCCATGTCTAGGAGAGTGGGTTGTCTAGACCTCTGGAGGCTTCCACCTCT 1148  
DB 2075 CTACCCCATGTCTAGGAGAGTGGGTTGTCTAGACCTCTGGAGGCTTCCACCTCT 2134  
QY 1149 GTCTCCCGAGCT 1208  
DB 2135 GTCTCCCGAGCT 2194  
QY 1209 GTAGTTTGTCTGTAAGAGTGTCTTTTGTATTTAATGCTGTGGCATGGTGAAGAG 1268  
DB 2195 GTAGTTTGTCTGTAAGAGTGTCTTTTGTATTTAATGCTGTGGCATGGTGAAGAG 2254  
QY 1269 GAGGGAAGAGGCTGTGTGGCT 1328  
DB 2255 GAGGGAAGAGGCTGTGTGGCT 2314  
QY 1329 CTCTGCTCTGTATCAGCCCAACCTCTGCTCTAGACACAGACAGACAGGAGAGAGCTCA 1388  
DB 2315 CTCTGCTCTGTATCAGCCCAACCTCTGCTCTAGACACAGACAGACAGGAGAGAGCTCA 2374  
QY 1389 GCTGCAATTCGAGGCT 1448  
DB 2375 GCTGCAATTCGAGGCT 2434  
QY 1449 GGGTAATAAAGTGGTGTGGGAAAAAAGAAAAAAGAAAAAAGAAAAA 1492  
DB 2435 GGGTAATAAAGTGGTGTGGGAAAAAAGAAAAAAGAAAAAAGAAAAA 2478

## RESULT 11

US-10-245-771-9  
; Sequence 9, Application US/10245771  
; Publication No. US20030068781A1

## GENERAL INFORMATION:

; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3630R1C98

; CURRENT APPLICATION NUMBER: US/10/245,771

; CURRENT FILING DATE: 2002-09-16

; PRIOR APPLICATION NUMBER: 10/197942

; PRIOR FILING DATE: 2002-07-18

; PRIOR APPLICATION NUMBER: 60/059114

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/063046

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/065027

; PRIOR FILING DATE: 1997-11-10

; PRIOR APPLICATION NUMBER: 60/079689

; PRIOR FILING DATE: 1998-03-27

; PRIOR APPLICATION NUMBER: 60/086478

; PRIOR FILING DATE: 1998-05-22

; PRIOR APPLICATION NUMBER: 60/087607

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/089801

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: 60/090557

; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: 60/090689

; PRIOR FILING DATE: 1998-06-25

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 116

; SEQ ID NO 9

; LENGTH: 2482

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-245-771-9

Query Match 97.5%; Score 1468; DB 15; Length 2482;

Best Local Similarity 99.3%; Pred. No. 0;

Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 9 CACGAGAGCAGATCTGCAAGAGTTTCGTTTATGAGGCTGCTTTGGGCAACAGAACAC 68

DB 995 CCCACGAGCAGATCTGCAAGAGTTTCGTTTATGAGGCTGCTTTGGGCAACAGAACAC 1054

QY 69 TACCTTGGGAAGAGAGTGCATTCAGCTCTGCGGGTGTGCAAGTGGGCTTTGAGA 128

DB 1055 TACCTTGGGAAGAGAGTGCATTCAGCTCTGCGGGTGTGCAAGTGGGCTTTGAGA 1114

QY 129 GCGAGCTCTGGGGCTCAGGGGCTTTCCCGAGGGCCCTTCCATGGAAGGCGCATCCA 188

DB 1115 GCGAGCTCTGGGGCTCAGGGGCTTTCCCGAGGGCCCTTCCATGGAAGGCGCATCCA 1174

QY 189 GTGTGCTCTGCACTGTTCAGCCCAACAGTTCGCTGCGAGCAATGGCTGTGATCGAC 248

DB 1175 GTGTGCTCTGCACTGTTCAGCCCAACAGTTCGCTGCGAGCAATGGCTGTGATCGAC 1234

QY 249 AGTTTCTCTGGAGTGTGAGCAGACCCCAACTGCGCCCGAGCGCTCCGACGAGGCTGCTGT 308

DB 1235 AGTTTCTCTGGAGTGTGAGCAGACCCCAACTGCGCCCGAGCGCTCCGACGAGGCTGCTGT 1294



Db 1115 GCGAGCTCTGGGCTCAGGCGACITTTCCCGAGGGCCCTCCAGGAAGGCGCATCCA 1174  
Qy 189 GTGTGCTCTGGGCACTCTCAGCCGACCCAGTTCGCTGCGCAGCAATGCTGCTGATGAC 248  
Db 1175 GTGTGCTCTGGGCACTCTCAGCCGACCCAGTTCGCTGCGCAGCAATGCTGCTGATGAC 1234  
Qy 249 AGTTTCCTGGAGTGTGAGACACCCGCAACCTGCGCGAGGCTCTCGAGAGGCTGCTGT 308  
Db 1235 AGTTTCCTGGAGTGTGAGACACCCGCAACCTGCGCGAGGCTCTCGAGAGGCTGCTGT 1294  
Qy 309 GAAATAATACAGAGTGTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAG 368  
Db 1295 GAAATAATACAGAGTGTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAG 1354  
Qy 369 CACTGCTGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCT 428  
Db 1355 CACTGCTGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCT 1414  
Qy 429 AACCCCTTCAGGAAACATGCGCCGCTTTTACTATGTTGGTGTGTTTACGGCAAGAAC 488  
Db 1415 AACCCCTTCAGGAAACATGCGCCGCTTTTACTATGTTGGTGTGTTTACGGCAAGAAC 1474  
Qy 489 AACTTTGAG 548  
Db 1475 AACTTTGAG 1534  
Qy 549 TTTGGCTCAGGCGGGAATCCCAATCCAGACAGAGCTCTGTGAGAGAGCTGTGCA 608  
Db 1535 TTTGGCTCAGGCGGGAATCCCAATCCAGACAGAGCTCTGTGAGAGAGCTGTGCA 1594  
Qy 609 GTGTCTCTGCTATCTGCAATGTTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 668  
Db 1595 GTGTCTCTGCTATCTGCAATGTTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1654  
Qy 669 AACGAGAGAGAGCTCTCAGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 728  
Db 1655 AACGAGAGAGAGCTCTCAGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1714  
Qy 729 ACTGTCTCCTACGAG 788  
Db 1715 ACTGTCTCCTACGAG 1774  
Qy 789 TGAGCTGGGTCTCAGCGGCTCTCAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 848  
Db 1775 TGAGCTGGGTCTCAGCGGCTCTCAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1834  
Qy 849 TGGGCTGGGAAAACTTTGGAACAGAGCTCTTGGCTGTTTCCAGGCGCCACTGTGCTCA 908  
Db 1835 TGGGCTGGGAAAACTTTGGAACAGAGCTCTTGGCTGTTTCCAGGCGCCACTGTGCTCA 1894  
Qy 909 GAGACAGAGGCTCCAGCCCTCTTGGAGAGCTCTGAGTAAGCTCACGCTCCTGAGAAAGC 968  
Db 1895 GAGACAGAGGCTCCAGCCCTCTTGGAGAGCTCTGAGTAAGCTCACGCTCCTGAGAAAGC 1954  
Qy 969 TCAAAGTTTGGAG 1028  
Db 1955 TCAAAGTTTGGAG 2014  
Qy 1029 CTTGATAGAGTTTGGAGAGAGTTGGAGTTTGGTTTCTCTCTCTCTCTCTCTCTCTCTCT 1088  
Db 2015 CTTGATAGAGTTTGGAGAGAGTTGGAGTTTGGTTTCTCTCTCTCTCTCTCTCTCTCTCT 2074  
Qy 1089 CTACCCCTAGTGTCTAGAGAGAGAGTGGGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1148  
Db 2075 CTACCCCTAGTGTCTAGAGAGAGAGTGGGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2134  
Qy 1149 GTCTCTCCGAGCT 1208  
Db 2135 GTCTCTCCGAGCT 2194  
Qy 1209 GTAGTTTGTCTGTAAAGAGTTGTTTGTGTTTAAATGCTGTGTCATGGGTGAAGAG 1268  
Db 2195 GTAGTTTGTCTGTAAAGAGTTGTTTGTGTTTAAATGCTGTGTCATGGGTGAAGAG 2254

Qy 1269 GAGGGAAGAGGCTCTTTGGCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1328  
Db 2255 GAGGGAAGAGGCTCTTTGGCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2314  
Qy 1329 CTCTGCTCTGATCAGCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1388  
Db 2315 CTCTGCTCTGATCAGCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2374  
Qy 1389 GCTGCAATTCGCGAGCGCCCAACCCCAAGGTTTCTTCAACATCAGAGCCGCGCCCACT 1448  
Db 2375 GCTGCAATTCGCGAGCGCCCAACCCCAAGGTTTCTTCAACATCAGAGCCGCGCCCACT 2434  
Qy 1449 GGTAATAAAGTGTGTTTGGTAATAAAGTGTGTTTGGTAATAAAGTGTGTTTGGTAATAA 1492  
Db 2435 GGTAATAAAGTGTGTTTGGTAATAAAGTGTGTTTGGTAATAAAGTGTGTTTGGTAATAA 2478

RESULT 13  
US-10-245-883-9  
; Sequence 9, Application US/10245883  
; Publication No. US20030068783A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Batson, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3630R1C70  
; CURRENT APPLICATION NUMBER: US/10/245,883  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining prior application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 9  
; LENGTH: 2482  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-245-883-9

Query Match 97.5%; Score 1468; DB 15; Length 2482;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 9 CACGAGGAGCAGATCTGCAAGAGTTTCTGTTTANGAGGCTCTTGGGCAACAGAACAC 68



995	Db	CCCACGGACGATCTCGACAGAGTTTCGTATTATGGAGGGCTGCTTGGCGAACAGAGAACAC	1054
69	QY	TACTCTTCGGGAAGAGAGTGCAATCTTAGCTCTTCGGGGTGTCCAAAGTGGGGCTTTGAGA	128
1055	Db	TACTCTTCGGGAAGAGAGTGCAATCTTAGCTCTTCGGGGTGTCCAAAGTGGGGCTTTGAGA	1114
129	QY	GGCAGCTCTGGGGCTCAGGCGACTTTCCGCCAGGGGCCCTCCATGGAAGAGGCCCATCCA	188
1115	Db	GGCAGCTCTGGGGCTCAGGCGACTTTCCGCCAGGGGCCCTCCATGGAAGAGGCCCATCCA	1174
189	QY	GTGTGCTCTGGCACCTGTTCAGCCCAACCCAGTTCGCGTCGACGAATGGCTGTGATCCGAC	248
1175	Db	GTGTGCTCTGGCACCTGTTCAGCCCAACCCAGTTCGCGTCGACGAATGGCTGTGATCCGAC	1234
249	QY	AGTTTCCTCGAGTGTGACGACACCCCAACTGCGCCCGACGCTTCGACGAGGCTCCCTGT	308
1235	Db	AGTTTCCTCGAGTGTGACGACACCCCAACTGCGCCCGACGCTTCGACGAGGCTCCCTGT	1294
309	QY	GAATAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCGACGACAAAGGG	368
1295	Db	GAATAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCGACGACAAAGGG	1354
369	QY	CACTCGCTGACCTGCCAGACACGAGCTCTGCAAGGAGAGCATCCCGCGCTGTGTACTAC	428
1355	Db	CACTCGCTGACCTGCCAGACACGAGCTCTGCAAGGAGAGCATCCCGCGCTGTGTACTAC	1414
429	QY	AACCCCTTCAGCAACACTGCGCCCGCTTTACTATGCTGTGTTTACGCGCAACAGAAC	488
1415	Db	AACCCCTTCAGCAACACTGCGCCCGCTTTACTATGCTGTGTTTATGGCAACAGAAC	1474
489	QY	AACCTTTGAGGAAGACGACGCTGCTCGAGTCTTGTTCGGGCATCTTCAAAGAGGATGTG	548
1475	Db	AACCTTTGAGGAAGACGACGCTGCTCGAGTCTTGTTCGGGCATCTTCAAAGAGGATGTG	1534
549	QY	TTTGGCTCAGGGGGGAAATCCCATTCGCCAGACAGGCTCTGTGGAGATGGCTGTGCA	608
1535	Db	TTTGGCTCAGGGGGGAAATCCCATTCGCCAGACAGGCTCTGTGGAGATGGCTGTGCA	1594
609	QY	GTGTTCTCTGCTCATCTGCATTTGTGGTGTGATAGCCATCTTGGGTTACTGCTTCTTCAAG	668
1595	Db	GTGTTCTCTGCTCATCTGCATTTGTGGTGTGATAGCCATCTTGGGTTACTGCTTCTTCAAG	1654
669	QY	AACCAGAGAAGAGACTTCCACGGACACCAACACCCACACCCACCCACCCCTGCGAGCTCC	728
1655	Db	AACCAGAGAAGAGACTTCCACGGACACCAACACCCACACCCACCCCTGCGAGCTCC	1714
729	QY	ACTGCTCTCATACCGAGGACACGAGACACTGGTCTATTAACACACACCGGGCCCTC	788
1715	Db	ACTGCTCTCATACCGAGGACACGAGACACTGGTCTATTAACACACACCGGGCCCTC	1774
789	QY	TGAGCTTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTGCTGTCGAAGGACAGAGGC	848
1775	Db	TGAGCTTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTGCTGTCGAAGGACAGAGGC	1834
849	QY	TGGCTTGGGAAAAACTTTTGGAAACGAGACTCTTGTGCTTTTCCAGGCCCATCTGTGCTCA	908
1835	Db	TGGCTTGGGAAAAACTTTTGGAAACGAGACTCTTGTGCTTTTCCAGGCCCATCTGTGCTCA	1894
909	QY	GAGACACGGGCTCAGCCCTCTCTTGGAGAGTCTCAGCTAAGTCTCAGTCTCTCAGAAAGC	968
1895	Db	GAGACACGGGCTCAGCCCTCTCTTGGAGAGTCTCAGCTAAGTCTCAGTCTCTCAGAAAGC	1954
969	QY	TCAAAGGTTTGGAAAGGACGAAAAACCTTTGGGCAGAACTACAGACTAGATGGACCTG	1028
1955	Db	TCAAAGGTTTGGAAAGGACGAAAAACCTTTGGGCAGAACTACAGACTAGATGGACCTG	2014
1029	QY	CTTGCAATGAGATTGGAGGAAGTTGGAGTTTGTCTCTGTTTCAAAGCTGCCTGTCC	1088
2015	Db	CTTGCAATGAGATTGGAGGAAGTTGGAGTTTGTCTCTGTTTCAAAGCTGCCTGTCC	2074
1089	QY	CTACCCCATGCTGTAGGAACAGGAGTGGGCTGTGTGACACCCCTGGAGGCCCAACCTT	1148

**RESULT 14**

US-10-237-535-9

US-10-237-333-3  
: Sequence 9. Application US/10237535

Publication No. IIS20030073188A1  
; sequence 9, Application US/1023

; Publication No. US20  
: GENERAL INFORMATION:

; GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Eaton, Dan

APPLICANT: Filvaroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT; Grimaldi, J. Chr.

APPLICANT: GURNEY, G.  
APPLICANT: Gurney, Austin

APPLICANT: GURNEY, AUSTIN  
APPLICANT: SMITH, VICTORIA

APPLICANT: SMITH, VICTORIA  
APPLICANT: Stephen, Jean-

APPLICANT: Stephan, Jean-

; APPLICANT: Watanbe, Coll

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEM

1. TITLE OF INVENTION: ACIDS ENCOD

; TITLE OF INVENTION: ACIDS ENCODING  
: TITLE REFERENCE: P3630R1C3

FILE REFERENCE: P363URIC3  
CURRENT APPLICATION NUMBER: IIS/10/2

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; CURRENT FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: 10/197942

; PRIOR FILING DATE: 2002-07-18

;; PRIOR APPLICATION NUMBER: 60/059114

PRIOR FILING DATE: 1997-09-17

; PRIOR FILING DATE: 1991-03-11;  
 : PRIOR APPLICATION NUMBER: 60/063046

;; PRIOR APPLICATION NUMBER: 80/003048  
: PRIOR FILING DATE: 1997-10-24



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PRIOR FILING DATE: 2001-08-13  
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; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 10/119480
; PRIOR FILING DATE: 2002-04-09

Query Match          97.5%; Score 1468; DB 15; Length 2482;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 9 CACGAGGACAGATCTGCAAGAGTTTCGTTTATGAGGCTGCTTGGGCAACAGAACAC 68
DB 995 CCCACGAGCAGATCTGCAAGAGTTTCGTTTATGAGGCTGCTTGGGCAACAGAACAC 1054

QY 69 TACCTTGGGGAAGAGAGTGCAATTCAGCTCTGCGGGGTGTGCAAGTGGGCTTTGAGA 128
DB 1055 TACCTTGGGGAAGAGAGTGCAATTCAGCTCTGCGGGGTGTGCAAGTGGGCTTTGAGA 1114

QY 129 GGCAGCTCTGGGCTCAGCGGACTTTCCCGAGGGCCCTCCATGGAAGGGCCATCCA 188
DB 1115 GGCAGCTCTGGGCTCAGCGGACTTTCCCGAGGGCCCTCCATGGAAGGGCCATCCA 1174

QY 189 GTGTGCTCTGGCAGCTGTGAGCCACCCAGTTCCGCTGCAAGATGGCTGTGCAAC 248
DB 1175 GTGTGCTCTGGCAGCTGTGAGCCACCCAGTTCCGCTGCAAGATGGCTGTGCAAC 1234

QY 249 AGTTTCTGTGAGTGACAGACACCCCACTGCGCGAGGCTTCGAGAGGCTGCTGT 308
DB 1235 AGTTTCTGTGAGTGACAGACACCCCACTGCGCGAGGCTTCGAGAGGCTGCTGT 1294

QY 309 GAAATAATACAGAGTGGCTTTGACGAGCTCCAGGCGATCCATTTCCCGACGACAAAGGG 368
DB 1295 GAAATAATACAGAGTGGCTTTGACGAGCTCCAGGCGATCCATTTCCCGAGGAGGG 1354

QY 369 CACTGTGTGAGCTGTGACAGACAGAGCTCTGCAAGAGAGAGATCCCGGCTGTACTAC 428
DB 1355 CACTGTGTGAGCTGTGACAGACAGAGCTCTGCAAGAGAGAGATCCCGGCTGTACTAC 1414

QY 429 AACCCCTTCAGGAAACACTGCGCGCTTTACTATGTTGTTTACGCAACAGAAC 488
DB 1415 AACCCCTTCAGGAAACACTGCGCGCTTTACTATGTTGTTTACGCAACAGAAC 1474

QY 489 AACTTTGAGGAAGAGCAGAGTGCCTCGAGTCTTTGTGCGGCGATCTCCAAGAGAGATGTG 548
DB 1475 AACTTTGAGGAAGAGCAGAGTGCCTCGAGTCTTTGTGCGGCGATCTCCAAGAGAGATGTG 1534

QY 549 TTTGGCTGAGGGGGAATCCCATTCAGCAGCAGGCTCTGTGGAGATGGCTGTGCA 608
DB 1535 TTTGGCTGAGGGGGAATCCCATTCAGCAGCAGGCTCTGTGGAGATGGCTGTGCA 1594

QY 609 GTGTCTCTGCTCATCTGCAATTTGGTGTGTGTAGCCATCTTGGGTTACTGTTTCTCAAG 668
DB 1595 GTGTCTCTGCTCATCTGCAATTTGGTGTGTGTAGCCATCTTGGGTTACTGTTTCTCAAG 1654

QY 669 AACGAGAAAGGACTTTCAGCGACACACACACACACACACACACACACACACACACAC 728
DB 1655 AACGAGAAAGGACTTTCAGCGACACACACACACACACACACACACACACACACACAC 1714

QY 729 ACTGTCTCCACTACGAGGACAGGAGCAGCTGTGTCTATAACACACACACACACACAC 788
DB 1715 ACTGTCTCCACTACGAGGACAGGAGCAGCTGTGTCTATAACACACACACACACACAC 1774

QY 789 TGAGCTGGGCTCTACCGGCTCTACCTGGGCTCTACCTGGGCTCTACCTGGGCTCTACCG 848
DB 1775 TGAGCTGGGCTCTACCGGCTCTACCTGGGCTCTACCTGGGCTCTACCTGGGCTCTACCG 1834

QY 849 TGCGCTGGGAAAACCTTTGCAACAGACTCTTGGCTGTGTTCCAGCGCCACTGTGCTCA 908
DB 1849 TGCGCTGGGAAAACCTTTGCAACAGACTCTTGGCTGTGTTCCAGCGCCACTGTGCTCA

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DB 1835 TGGGCTGGAAAAAATTTTGGAAACAGACTCTTGCTCTGTTTCCAGGCCACCTGTGCTCA 1894
QY 909 GAGACACGGGCTGACAGCCCTCTTGGAGAGTCTCAGCTAGAGCTCAGCTCTGAGAAAGC 968
DB 1895 GAGACACGGGCTGACAGCCCTCTTGGAGAGTCTCAGCTAGAGTCACTGCTGAGAAAGC 1954
QY 969 TCAAAGGTTTGGAAAGGAGCAGAAAAACCTTGGGCCAGAAAGTACCAGACTAGATGAGACTG 1028
DB 1955 TCAAAGGTTTGGAAAGGAGCAGAAAAACCTTGGGCCAGAAAGTACCAGACTAGATGAGACTG 2014
QY 1029 CCTGCAATAGGAGTTTGGAGGAAGTTGGAGTTTGTCTCTCTCTCTCAAGCTGCTGCTCC 1088
DB 2015 CCTGCAATAGGAGTTTGGAGGAAGTTGGAGTTTGTCTCTCTCTCTCAAGCTGCTGCTCC 2074
QY 1089 CTACCCCATGCTGTAGGAAGAGAGTGGGTGTGTGAGACCTCTGGAGGGCCCAACCCCT 1148
DB 2075 CTACCCCATGCTGTAGGAAGAGAGTGGGTGTGTGAGACCTCTGGAGGGCCCAACCCCT 2134
QY 1149 GTCTCTCCGAGCTCTCTTCCATGCTGTGCGCCAGAGGCTGGAGGAAGGACTTCCCTGT 1208
DB 2135 GTCTCTCCGAGCTCTCTTCCATGCTGTGCGCCAGAGGCTGGAGGAAGGACTTCCCTGT 2194
QY 1209 GTAGTTTGTCTGTAAAGAGTTGCTTTTGTATTTAATGCTGTGGCATGGGTGAAGAG 1268
DB 2195 GTAGTTTGTCTGTAAAGAGTTGCTTTTGTATTTAATGCTGTGGCATGGGTGAAGAG 2254
QY 1269 GAGGGGAAGAGGCTGTGTGCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1328
DB 2255 GAGGGGAAGAGGCTGTGTGCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2314
QY 1329 CTCTGCCCTTCATCAGCCCGCCACCTGGCTAGACAGCAGACAGAGCCAGAGAGCTCA 1388
DB 2315 CTCTGCCCTTCATCAGCCCGCCACCTGGCTAGACAGCAGAGCCAGAGAGCTCA 2374
QY 1389 GCTGCAATTCGAGCCCGCCACCTGGCTAGACAGCAGAGCTTCTCCAAATCAGAGCCCGCCACT 1448
DB 2375 GCTGCAATTCGAGCCCGCCACCTGGCTAGACAGCAGAGCTTCTCCAAATCAGAGCCCGCCACT 2434
QY 1449 GCGTAATTAAGTGGTTGTGGAAGAAAAAAGAAAAAAGAAAAA 1492
DB 2435 GCGTAATTAAGTGGTTGTGGAAGAAAAAAGAAAAAAGAAAAA 2478

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RESULT 15
US-10-238-183-9
; Sequence 9, Application US/10238183
; Publication No. US20030073189A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaud, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C11
; CURRENT APPLICATION NUMBER: US/10/238,183
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10

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 , PRIOR APPLICATION NUMBER: 09/403297  
 , PRIOR FILING DATE: 1999-10-18  
 , PRIOR APPLICATION NUMBER: 09/423741  
 , PRIOR FILING DATE: 1999-11-10  
 , PRIOR APPLICATION NUMBER: 09/709238  
 , PRIOR FILING DATE: 2000-11-08

[illegible]

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2004, 00:39:17 ; Search time 636 Seconds  
(without alignments)  
10052.733 Million cell updates/sec

Title: US-09-935-390A-4  
Perfect score: 1505  
Sequence: 1 GAATTCGGCAGGAGCAG.....AAAAAGTCTGGGGCCGC 1505

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 337363 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq 29Jan04:.\*  
1: geneseq1980s:.\*  
2: geneseq1990s:.\*  
3: geneseq2000s:.\*  
4: geneseq2001as:.\*  
5: geneseq2001bs:.\*  
6: geneseq2002s:.\*  
7: geneseq2003as:.\*  
8: geneseq2003bs:.\*  
9: geneseq2003cs:.\*  
10: geneseq2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1505	100.0	1505	2	Aav43604 Human sec
2	1468	97.5	2482	4	Aaf30055 Human cDN
3	1468	97.5	2482	4	Adl16721 Human hep
4	1468	97.5	2482	6	Abk40259 CDNA enco
5	1468	97.5	2482	6	AbL88092 Human PRO
6	1468	97.5	2482	6	AbK69965 CDNA enco
7	1468	97.5	2482	6	AbL95581 Human ang
8	1468	97.5	2482	6	Ada01277 Human PRO
9	1468	97.5	2482	8	Ada43706 Human cDN
10	1468	97.5	2482	8	Ada43474 Human PRO
11	1468	97.5	2482	8	Ada01149 Human PRO
12	1468	97.5	2482	8	Ada01033 Human cDN
13	1468	97.5	2482	8	Ada43590 Human PRO
14	1468	97.5	2482	8	Ada06852 Human PRO
15	1468	97.5	2482	8	Ada08340 Novel hum
16	1468	97.5	2482	8	AbB99633 Human PRO
17	1468	97.5	2482	8	AbB66916 Human PRO
18	1468	97.5	2482	8	AbB66071 Human cDN
19	1468	97.5	2482	9	AbB99749 Human PRO
20	1468	97.5	2482	9	AbB99404 Novel hum
21	1468	97.5	2482	9	AbB65955 Human cDN
22	1468	97.5	2482	9	AdC23353 Human cDN
23	1468	97.5	2482	9	AdC26046 Human PRO

24	1468	97.5	2482	9	ADD10330	Add10330 Human sec
25	1468	97.5	2482	9	ADD11290	Add11290 Human sec
26	1468	97.5	2482	9	ADD37083	Add37083 Human sec
27	1468	97.5	2482	9	ADG04873	AdG04873 Human PRO
28	1468	97.5	2482	9	ADG11179	AdG11179 Human PRO
29	1468	97.5	2482	9	ADD88110	Add88110 Human PRO
30	1468	97.5	2482	9	ADD95405	Add95405 Human PRO
31	1468	97.5	2482	9	ADG06335	AdG06335 Human PRO
32	1468	97.5	2482	9	ADG38110	AdG38110 Human PRO
33	1468	97.5	2482	9	ADD88226	Add88226 Human PRO
34	1468	97.5	2482	9	ADD90807	Add90807 Human cDN
35	1468	97.5	2482	10	ADE51660	AdE51660 Human cDN
36	1468	97.5	2482	10	ADE51776	AdE51776 Human cDN
37	1468	97.5	2482	10	ADE37634	AdE37634 Human cDN
38	1468	97.5	2482	10	ADE37518	AdE37518 Human cDN
39	1468	97.5	2482	10	ADD95289	Add95289 Human cDN
40	1468	97.5	2482	10	ADE37989	AdE37989 Human PRO
41	1468	97.5	2482	10	ADE76078	AdE76078 Human PRO
42	1468	97.5	2482	10	ADE39401	AdE39401 Human PRO
43	1468	97.5	2482	10	ADG04205	AdG04205 Human PRO
44	1468	97.5	2482	10	ADG39802	AdG39802 Human PRO
45	1468	97.5	2482	10	ADE19667	AdE19667 Human PRO

## ALIGNMENTS

RESULT 1  
AAV43604  
ID AAV43604 standard; DNA; 1505 BP.  
XX  
AC AAV43604;  
XX  
DT 24-SEP-1998 (first entry)  
XX  
DE Human secreted protein 4 encoding DNA.  
XX  
KW Secreted protein; human; cell proliferation; cytokine activity;  
KW tissue growth; cellular differentiation; regeneration; activin; inhibin;  
KW chemotactic; haemostatic; thrombolytic; tumour inhibition;  
KW anti-inflammatory activity; biomarker; ss.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 171..791  
FT /\*tag= a  
FT /product= "human secreted protein"  
XX  
FN WO9825959-A2.  
XX  
PD 18-JUN-1998.  
XX  
PF 11-DEC-1997; 97WO-US022787.  
XX  
PR 11-DEC-1996; 96US-0032757P.  
XX (CHIR ) CHIRON CORP.  
XX  
PI Escobedo J, Hu Q, Garcia P, Williams LT, Kothakota S;  
XX  
DR WPI; 1998-348453/30.  
DR P-PSDB; AAW63684.  
XX  
FT Secreted human polypeptides - having cytokine, cell proliferation or  
FT differentiation, activin or inhibin, tumour inhibition or anti-  
FT inflammatory activities.  
XX  
PS Claim 6; Page 31-32; 78pp; English.  
XX  
CC This DNA encodes a human secreted protein. The specification provides  
CC secreted protein sequences (AAW63681 to AAW63699) encoded by the nucleic  
CC acid sequences shown in AAV43601 to AAV43619. The invention provides a









Qy 609 GTGTTCTGTCATCTGCAATGTGGTGTGGTGTAGGCATCTTGGGTACTTGTCTTCAAG 668  
 Db 1595 GTGTTCTGTCATCTGCAATGTGGTGTGGTGTAGGCATCTTGGGTACTTGTCTTCAAG 1654  
 Qy 669 AACCAGAGAAAGGACTTCCAGGACACCCACACACACACACACACACACACACACACAC 728  
 Db 1655 AACCAGAGAAAGGACTTCCAGGACACCCACACACACACACACACACACACACACACAC 1714  
 Qy 729 ACTGTCTCCATACCGAGGACACCGGACACCTGTCTATACGACACACCGGCGCCCTC 788  
 Db 1715 ACTGTCTCCATACCGAGGACACCGGACACCTGTCTATACGACACACCGGCGCCCTC 1774  
 Qy 789 TGAGCTGGGTCTCACCGGCTCTACCTGGGCTCTCTGCTTCCAGGACAGAGGAC 848  
 Db 1775 TGAGCTGGGTCTCACCGGCTCTCACCTGGGCTCTCTGCTTCCAGGACAGAGGAC 1834  
 Qy 849 TGGGCTGGGAAAAAATTTGGAAACGAGCTTGTGCTTCCAGGACACCTGTGCTCA 908  
 Db 1835 TGGGCTGGGAAAAAATTTGGAAACGAGCTTGTGCTTCCAGGACACCTGTGCTCA 1894  
 Qy 909 GAGACAGGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCACCTCTGAGAAAGC 968  
 Db 1895 GAGACAGGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCACCTCTGAGAAAGC 1954  
 Qy 969 TCAAAGGTTTGGAGGACAGAAACCTTGGGCGCAGAGTACAGACTAGATGACCTG 1028  
 Db 1955 TCAAAGGTTTGGAGGACAGAAACCTTGGGCGCAGAGTACAGACTAGATGACCTG 2014  
 Qy 1029 CCTCATAGGAGTTGGAGGAGTTGGAGTTTGTCTCTGTTTCAAGCTGCTCTCC 1088  
 Db 2015 CCTCATAGGAGTTGGAGGAGTTGGAGTTTGTCTCTGTTTCAAGCTGCTCTCC 2074  
 Qy 1089 CTACCCCATGTTGTAGGAGGAGTGGGCTGTGTGAGCCCTTGGAGGCGCCCAACCT 1148  
 Db 2075 CTACCCCATGTTGTAGGAGGAGTGGGCTGTGTGAGCCCTTGGAGGCGCCCAACCT 2134  
 Qy 1149 GTCTCCCGAGCTCTCTTCCATGCTGTGCGCCACAGGCTGGAGAGGACTTCCCTGT 1208  
 Db 2135 GTCTCCCGAGCTCTCTTCCATGCTGTGCGCCACAGGCTGGAGAGGACTTCCCTGT 2194  
 Qy 1209 GTAGTTTGTCTGTAAGAGTTGCTTTTGTATTTAATGCTGTGGCATGGGTGAAGAG 1268  
 Db 2195 GTAGTTTGTCTGTAAGAGTTGCTTTTGTATTTAATGCTGTGGCATGGGTGAAGAG 2254  
 Qy 1269 GAGGGAAGAGGCTTGTGGCTCTCTATCTCTCTTCTTCTTCCCTTCCCTTCCCTTCCCT 1328  
 Db 2255 GAGGGAAGAGGCTTGTGGCTCTCTATCTCTCTTCTTCTTCCCTTCCCTTCCCTTCCCT 2314  
 Qy 1329 CTCTGCTTGTATCAGCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 1388  
 Db 2315 CTCTGCTTGTATCAGCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 2374  
 Qy 1389 GCTGATTCGAGCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 1448  
 Db 2375 GCTGATTCGAGCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 2434  
 Qy 1449 GGGTAATAAAGTGGTTGTGGAAAAAATTTGGAAAAAATTTGGAAAAAATTTGGAAAAA 1492  
 Db 2435 GGGTAATAAAGTGGTTGTGGAAAAAATTTGGAAAAAATTTGGAAAAAATTTGGAAAAA 2478

RESULT 4

ID ABK40259 standard; cDNA; 2482 BP.  
 XX  
 AC ABK40259;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DZ cDNA encoding human PR0256 polypeptide.  
 XX  
 KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;

KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;  
 KW inflammatory disorder; immune disorder; angiogenic disorder;  
 KW gene therapy; cytostatic; neuroprotective; gene; ss.  
 OS Homo sapiens.  
 PN WO200153486-A1.  
 XX 26-JUL-2001.  
 XX 11-FEB-2000; 2000WO-US003565.  
 PF 08-MAR-1999; 99WO-US005028.  
 PR 11-MAR-1999; 99US-0123972P.  
 PR 11-MAY-1999; 99US-0133459P.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 22-JUN-1999; 99US-0140650P.  
 PR 20-JUL-1999; 99US-0140653P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 28-JUL-1999; 99US-0146222P.  
 PR 17-AUG-1999; 99US-0149395P.  
 PR 31-AUG-1999; 99US-0151489P.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 05-JAN-2000; 2000WO-US000219.  
 XX (SETH ) GENENTECH INC.  
 PA Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;  
 PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;  
 PI Matanabe CK, Wood WI;  
 XX MPI; 2002-205567/26.  
 DR P-PSDB; AAU86133.  
 XX Thirty five nucleic acids encoding PRO polypeptides, useful for treating  
 PT benign or malignant tumors, leukemias and lymphoid malignancies,  
 PT inflammatory, angiogenic and immunologic disorders.  
 XX Claim 50; Fig 11; 302pp; English.  
 XX The present invention relates to the isolation of novel human PRO  
 CC polypeptides and the polynucleotide sequences encoding them. The PRO  
 CC polypeptides, agonists, antagonists or anti-PRO antibodies are useful for  
 CC treating benign or malignant tumours (e.g. renal, kidney, bladder,  
 CC breast, etc), leukemias and lymphoid malignancies, other disorders such  
 CC as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,  
 CC stromal and blastocoele disorders, inflammatory, immune and angiogenic  
 CC disorders. The polynucleotide sequences are also useful in gene therapy.  
 CC ABK40254-ABK40288 encode for the human PRO polypeptides of the invention  
 XX  
 SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;  
 Query Match 97.5%; Score 1468; DB 6; Length 2482;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 Qy 9 CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGAGAGTCTTGGGCAACAGAACAC 68  
 Db 995 CCCACGAGCAGATCTGCAAGAGTTTCGTTTATGAGAGTCTTGGGCAACAGAACAC 1054  
 Qy 69 TACCTTCGGGAAGAGTCTAGCTCTGCGGCTGTCAGAGTGGGCTTTGAGA 128  
 Db 1055 TACCTTCGGGAAGAGTCTAGCTCTGCGGCTGTCAGAGTGGGCTTTGAGA 1114  
 Qy 129 GGCAGCTCTGGGCTCAGGCGACTTTTCCCGGAGGCTTCCATGGAAGAGCGCCATCCA 188  
 Db 1115 GGCAGCTCTGGGCTCAGGCGACTTTTCCCGGAGGCTTCCATGGAAGAGCGCCATCCA 1174

189 GTGCTCTGGCACTGTGACAGCCACCCAGTTCCTGCTGAGCAATGGCTGCTGATCGAC 248  
 1175 GTGTGCTCTGGCACTGTGACAGCCACCCAGTTCCTGCTGAGCAATGGCTGCTGATCGAC 1234  
 249 ACTTTCCTGGAGTGTGACAGCAACCCCAACTCCGCCGAGCGCTCCGAGAGGCTCCCTGT 308  
 1235 AGTTTCCTGGAGTGTGACAGCAACCCCAACTCCGCCGAGCGCTCCGAGAGGCTCCCTGT 1294  
 309 GAABAATACAGAGTGGCTTTCAGAGAGCTCCAGAGAGCATCCATTTCCCGAGGACAAAGGG 368  
 1295 GAAAAATACAGAGTGGCTTTCAGAGAGCTCCAGAGAGCATCCATTTCCCGAGTACAAAGGG 1354  
 369 CACTGCTGGAGCTTTCAGAGAGCTCCAGAGAGCATCCCGGCTGGTACTAC 428  
 1355 CACTGCTGGAGCTTTCAGAGAGCTCCAGAGAGCATCCCGGCTGGTACTAC 1414  
 429 AACCCCTTCAGAGAGCTTTCAGAGAGCTCCAGAGAGCATCCCGGCTGGTACTAC 488  
 1415 AACCCCTTCAGAGAGCTTTCAGAGAGCTCCAGAGAGCATCCCGGCTGGTACTAC 1474  
 489 AACTTTGAG 548  
 1475 AACTTTGAG 1534  
 549 TTGGCTTCAG 608  
 1535 TTGGCTTCAG 1594  
 609 GTGTTCTCTGATCATGCAATGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 668  
 1595 GTGTTCTCTGATCATGCAATGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1654  
 669 AACCAAG 728  
 1655 AACCAAG 1714  
 729 ACTGTCTCCACTACAG 788  
 1715 ACTGTCTCCACTACAG 1774  
 789 TGAGCTTGGCTCTCACCGGCTCTCACCGGCTCTCACCGGCTCTCACCGGCTCTCACCGGCT 848  
 1775 TGAGCTTGGCTCTCACCGGCTCTCACCGGCTCTCACCGGCTCTCACCGGCTCTCACCGGCT 1834  
 849 TGAGCTTGGCTCTCACCGGCTCTCACCGGCTCTCACCGGCTCTCACCGGCTCTCACCGGCT 908  
 1835 TGAGCTTGGCTCTCACCGGCTCTCACCGGCTCTCACCGGCTCTCACCGGCTCTCACCGGCT 1894  
 909 GAGACAGAGGCTCCAGCCCTCTTGGAGAGAGTCTCAGCTAAGCTCAGCTAAGCTCAGCTAAG 968  
 1895 GAGACAGAGGCTCCAGCCCTCTTGGAGAGAGTCTCAGCTAAGCTCAGCTAAGCTCAGCTAAG 1954  
 969 TCAAGGTTTGGAG 1028  
 1955 TCAAGGTTTGGAG 2014  
 1029 CCTGCTAGAGAGTGTGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 1088  
 2015 CCTGCTAGAGAGTGTGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 2074  
 1089 CTACCCCATGCTCTAGAGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 1148  
 2075 CTACCCCATGCTCTAGAGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 2134  
 1149 GTCTCCCGAGCTCTCTCCAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 1208  
 2135 GTCTCCCGAGCT 2194  
 1209 GTAGTTTGTGCTGTAAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1268  
 2195 GTAGTTTGTGCTGTAAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 2254  
 1269 GAGGGAG 1328

2255 GAGGGAG 2314  
 1329 CTCTGCTCTGATCATGAG 1388  
 2315 CTCTGCTCTGATCATGAG 2374  
 1389 GCTCATTTCCGAG 1448  
 2375 GCTCATTTCCGAG 2434  
 1449 GGGTAATAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1492  
 2435 GGGTAATAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2478

RESULT 5  
 ABL88092  
 ID ABL88092 standard; cDNA; 2482 BP.  
 XX  
 AC ABL88092;  
 DT 16-MAY-2002 (first entry)  
 XX  
 DE Human PRO256 cDNA sequence SEQ ID NO:41.  
 XX  
 KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
 KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 KW age-related macular degeneration; arterial restenosis; angina;  
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KW wound healing; chromosome mapping; gene mapping; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200200690-A2.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PF 20-JUN-2001; 2001WO-US019692.  
 XX  
 PR 23-JUN-2000; 2000US-0213637P.  
 PR 20-JUL-2000; 2000US-0219556P.  
 PR 25-JUL-2000; 2000US-0220624P.  
 PR 25-JUL-2000; 2000US-0220664P.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 02-AUG-2000; 2000US-0222695P.  
 PR 17-AUG-2000; 2000US-00643657.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 07-SEP-2000; 2000US-0230978P.  
 PR 18-SEP-2000; 2000US-00664610.  
 PR 18-SEP-2000; 2000US-00665350.  
 PR 24-OCT-2000; 2000US-0242922P.  
 PR 08-NOV-2000; 2000US-00709238.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000US-00747259.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PR 22-JAN-2001; 2001US-00767609.  
 PR 28-FEB-2001; 2001US-00796498.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 09-MAR-2001; 2001US-00802706.  
 PR 14-MAR-2001; 2001US-00808689.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 25-MAY-2001; 2001US-00866028.

PR	25-MAY-2001; 2001US-00866034.
PR	30-MAY-2001; 2001WO-US017092.
PR	35-MAY-2001; 2001US-00870574.
PR	30-MAY-2001; 2001WO-US017443.
XX	01-JUN-2001; 2001WO-US017800.
PA	(GSEH ) GENENTECH INC.
XX	Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI	Godowski PJ, Gurney AL, Hillan KJ, Marsters SH, Pan J, Paoni NF;
PI	Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX	
DR	WPI; 2002-090516/12.
DR	P-PDB; ABB84837.
XX	
PT	One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT	useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT	infarction), endothelial or angiogenic disorders in a mammal.
XX	
PS	Claim 2; Fig 41; 565pp; English.
XX	
CC	ABL8072 to ABL8258 encode the PRO proteins given in ABB84817 to
CC	ABB85003. The PRO proteins and polynucleotides have cardiac, cytostatic,
CC	antiangiogenic, hypotensive, vulnary and antiarteriosclerotic
CC	activities, and can be used in gene therapy. The PRO polynucleotides,
CC	proteins, agonists and antagonists are useful for treating or diagnosing
CC	a cardiovascular, endothelial or angiogenic disorder in a mammal e.g.
CC	cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC	atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC	angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC	angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC	healing. The PRO polynucleotides have applications in molecular biology,
CC	including use as hybridisation probes, and in chromosome and gene
CC	mapping. ABL8259 to ABL8267 represent primers and probes used in the
CC	exemplification of the present invention
XX	
SQ	Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;
	Query Match 97.5%; Score 1468; DB 6; Length 2482;
	Best Local Similarity 99.3%; Pred. No. 0;
	Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY	9 CACGAGGACGATCTCGAAGATTTCCTTATGAGGGTGCTTTGGGCACAAGAACAAC 68
Db	995 CCCACGAGCAGATCTCGAAGATTTCGTATTATGAGGGTGCTTTGGGCACAAGAACAAC 1054
QY	69 TACTCTCGGAAGAAGATGTCATTCTAGCCTGTGGGGTGTCGAAGTGCGCTTTTGAGA 128
Db	1055 TACTTTCGGAGAGAGTAGTGCATTTAGCCTGTTCGGGGTGTCGAAGTGCGCTTTTGAGA 1114
QY	129 GGCACTCTTGGGGCTCAGGGCGACTTTTCCCACAGGGGCCCTTCCATGGAAGAGCGCCATCCA 188
Db	1115 GGCACTCTTGGGGCTCAGGGCGACTTTTCCCCAGGGGCCCTTCCATGGAAGAGCGCCATCCA 1174
QY	189 GTGTGCTCTGGCACCTGTTCAGGCCACCAGTCGGCTGACGACCATGCTCTGCATCGAC 248
Db	1175 GTGTGCTCTGGCACCTGTTCAGGCCACCAGTCGGCTGACGACCATGCTCTGCATCGAC 1234
QY	249 AGTTTTCTTGGAGTGTGACGACACCCCCAACTGCCGCCGACGCTTCCGACGAGGCTGCCTGT 308
Db	1235 AGTTTTCTTGGAGTGTGACGACACCCCCAACTGCCGCCGACGCTTCCGACGAGGCTGCCTGT 1294
QY	309 GAATAATACACGAGTGGCTTTGACGAGCTCAGGGCATTCATTTCGCCAGGACGAAGGG 368
Db	1295 GAATAATACACGAGTGGCTTTGACGAGCTCAGGGCATTCATTTCGCCAGGACGAAGGG 1354
QY	369 CACTGCGTGACCTGACGACACACGAGACTCTGCAAGGAGAGACTCCCGCGCTGTACTAC 428
Db	1355 CACTGCGTGACCTGACGACACACGAGACTCTGCAAGGAGAGAGACTCCCGCGCTGTACTAC 1414
QY	429 AACCCCTTCACGGAACACTCGCCCGCTTTACCTATGGTGTGTGTACGGCAACAAGAAC 488
Db	1415 AACCCCTTCACGGAACACTCGCCCGCTTTACCTATGGTGTGTGTATGCAACAAGAAC 1474

XX AC ABK69965;  
 XX DT 15-JUL-2002 (first entry)  
 XX DE cDNA encoding human Pro peptide #5.  
 XX DX Human; ss; gene; PRO; secreted protein; transmembrane protein;  
 XX KW genetic disorder; tumour; cancer.  
 XX OS Homo sapiens.  
 XX PN WO200224888-A2.  
 XX PD 28-MAR-2002.  
 XX PF 29-AUG-2001; 2001WO-US027099.  
 XX PR 01-SEP-2000; 2000US-0229896P.  
 XX PR 05-SEP-2000; 2000US-0230621P.  
 XX PR 22-SEP-2000; 2000US-0235147P.  
 XX PR 10-NOV-2000; 2000WO-US030873.  
 XX PR 12-JAN-2001; 2001US-0261878P.  
 XX PR 16-JAN-2001; 2001US-0261910P.  
 XX PR 16-JAN-2001; 2001US-0261939P.  
 XX PR 16-JAN-2001; 2001US-0262150P.  
 XX PR 25-JAN-2001; 2001US-0264395P.  
 XX PR 02-FEB-2001; 2001US-0266421P.  
 XX PR 08-FEB-2001; 2001US-0267623P.  
 XX PR 28-FEB-2001; 2001WO-US006520.  
 XX PR 09-MAR-2001; 2001US-0274399P.  
 XX PR 03-APR-2001; 2001US-0280982P.  
 XX PR 04-APR-2001; 2001US-0282129P.  
 XX PR 04-APR-2001; 2001US-0282199P.  
 XX PR 09-MAY-2001; 2001US-0290589P.  
 XX PR 25-MAY-2001; 2001WO-US017052.  
 XX PR 01-JUN-2001; 2001WO-US017800.  
 XX PR 20-JUN-2001; 2001WO-US019692.  
 XX PR 29-JUN-2001; 2001WO-US021066.  
 XX PR 09-JUL-2001; 2001WO-US021735.  
 XX PR (GETH ) GENENTECH INC.  
 XX PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
 XX PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;  
 XX PI Fong S;  
 XX DR WPI: 2002-362426/39.  
 XX DR P-PSDB; ABG34034.  
 XX PT New PRO polypeptides and polynucleotides encoding the polypeptides,  
 XX PT useful in gene therapy, chromosome identification, tissue typing, or for  
 XX PT genetic analysis of individuals with genetic disorders.  
 XX PS Claim 2; Fig 9; 218pp; English.  
 XX CC This invention relates to the cDNA and protein sequences of novel  
 XX CC secreted and transmembrane polypeptides PRO polypeptides. The invention  
 XX CC also comprises a method for producing the proteins of the invention by  
 XX CC recombinant means and antibodies specific for the protein of the  
 XX CC invention. The antibody may be used for detecting the PRO proteins of the  
 XX CC invention and may be used to modify their activity. polynucleotides may  
 XX CC be used as hybridisation probes for a cDNA library to isolate the full-  
 XX CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation  
 XX CC probes for mapping the gene which encodes that PRO and for genetic  
 XX CC analysis of individuals with genetic disorders, in assays to identify  
 XX CC other proteins or molecules involved in binding reaction, to generate  
 XX CC transgenic animals or knock-out animals which in turn are useful in the  
 XX CC development and screening of therapeutically useful reagents, for  
 XX CC chromosome identification, and tissue typing. The PRO polypeptides are  
 XX CC useful in gene therapy, and as molecular weight markers for protein  
 XX CC electrophoresis purposes. The sequences may also be used to detect  
 XX CC overexpression on PRO polypeptides in cancerous tumours and for screening

CC for differentially expressed genes using microarray technology. The  
 CC present sequence represents a cDNA encoding a human PRO protein of the  
 CC invention  
 XX CC  
 XX SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;  
 Query Match 97.5%; Score 1468; DB 6; Length 2482;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 QY 9 CACGAGGAGCAGATCTGCAAGAGTTTGGTTATGAGGCTGTTGGGCAACAGAACAC 68  
 DB 995 CCCACGGAGCAGATCTGCAAGAGTTTGGTTATGAGGCTGTTGGGCAACAGAACAC 1054  
 QY 69 TACCTTCGGAGAGAGTGCATTTAGCTTCGGGTGTCAGAGTGGGCTTTGACA 128  
 DB 1055 TACCTTCGGAGAGAGTGCATTTAGCTTCGGGTGTCAGAGTGGGCTTTGACA 1114  
 QY 129 GGCAGCTTTGGGGCTCAGGCGACTTTCCCCAGAGGCCCTCCATGGAAGGGCCCATCCA 188  
 DB 1115 GGCAGCTTTGGGGCTCAGGCGACTTTCCCCAGAGGCCCTCCATGGAAGGGCCCATCCA 1174  
 QY 189 GTGTGCTTGGCACTGTGAGCCCAACCCAGTTCCGCTGAGCAATGGCTGTGCTGAC 248  
 DB 1175 GTGTGCTTGGCACTGTGAGCCCAACCCAGTTCCGCTGAGCAATGGCTGTGCTGAC 1234  
 QY 249 AGTTTCTGGAGTGTGAGACACCCCAACTGCCCCGAGCCTCCGACGAGCTGCTGT 308  
 DB 1235 AGTTTCTGGAGTGTGAGACACCCCAACTGCCCCGAGCCTCCGACGAGCTGCTGT 1294  
 QY 309 GAAAAATACAGAGTGGCTTTGACGAGCTTCAGCGCATCCATTTCCCGACGCAAAAGGG 368  
 DB 1295 GAAAAATACAGAGTGGCTTTGACGAGCTTCAGCGCATCCATTTCCCGACGCAAAAGGG 1354  
 QY 369 CACTGGGTGGACCTGCCAGACACAGACTCTGCAAGGAGAGCATCCCGGCTGTACTAC 428  
 DB 1355 CACTGGGTGGACCTGCCAGACACAGACTCTGCAAGGAGAGCATCCCGGCTGTACTAC 1414  
 QY 429 AACCCTTTGAGGAAACATGCGCCCGCTTTACTATGGTGGTGTTCAGGCAACAGAAC 488  
 DB 1415 AACCCTTTGAGGAAACATGCGCCCGCTTTACTATGGTGGTGTTCAGGCAACAGAAC 1474  
 QY 489 AACTTTGAGGAGAGCAGAGTGCCTCGAGTCTTTCGGGCGATCTCCAGAGAGATGTG 548  
 DB 1475 AACTTTGAGGAGAGCAGAGTGCCTCGAGTCTTTCGGGCGATCTCCAGAGAGATGTG 1534  
 QY 549 TTGGCTTGAGGCGGAAATCCCATTCAGCAGACAGGCTCTGTGGAGATGCTCTGCA 608  
 DB 1535 TTGGCTTGAGGCGGAAATCCCATTCAGCAGACAGGCTCTGTGGAGATGCTCTGCA 1594  
 QY 609 GTGTTCCTGCTCATCTGCATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 668  
 DB 1595 GTGTTCCTGCTCATCTGCATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1654  
 QY 669 AACCAGAGAAAGGACTTCCAGGACACACACACACACACACACACACACACACACAC 728  
 DB 1655 AACCAGAGAAAGGACTTCCAGGACACACACACACACACACACACACACACACACAC 1714  
 QY 729 ACTGTCTCCACTACCGAGGACACGAGCACTGTGTGTGTGTGTGTGTGTGTGTGTGT 788  
 DB 1715 ACTGTCTCCACTACCGAGGACACGAGCACTGTGTGTGTGTGTGTGTGTGTGTGTGT 1774  
 QY 789 TGAGGCTGGGTCTCACCGGCTCTCACCTGGGCGCTCTCTCTCTCTCTCTCTCTCTCTCT 848  
 DB 1775 TGAGGCTGGGTCTCACCGGCTCTCACCTGGGCGCTCTCTCTCTCTCTCTCTCTCTCTCT 1834  
 QY 849 TGGGCTGGGAAAAAATTTTGGAAACAGACTTTTGGCTGTTCAGGCGCCACTGTGCTCA 908  
 DB 1835 TGGGCTGGGAAAAAATTTTGGAAACAGACTTTTGGCTGTTCAGGCGCCACTGTGCTCA 1894  
 QY 909 GAGACAGGCTTCAGGCGCT 968  
 DB 1895 GAGACAGGCTTCAGGCGCT 1954



QY 69 TACTTTCGGGAAAGAGTGCATTCTAGCCTGTGGGGTGTGCAAGGTGGGCTTTGAGA 128  
Db 1055 TACTTTCGGGAAAGAGAGTGCATTCTAGCCTGTGGGGTGTGCAAGGTGGGCTTTGAGA 1114  
QY 129 GGCAGCTCTGGGCTCAGGCGCATTTTCCCGCCAGGCGCCCTTCCATGGAAGAGGCGCCCATCA 188  
Db 1115 GGCAGCTCTGGGCTCAGGCGCATTTTCCCGCCAGGCGCCCTTCCATGGAAGAGGCGCCCATCA 1174  
QY 189 GTGTGCTCTGGACCTGTAGCCCAAGCCAGTTCGCTGAGCAATGCTGCTGCTGCTGAGC 248  
Db 1175 GTGTGCTCTGGACCTGTAGCCCAAGCCAGTTCGCTGAGCAATGCTGCTGCTGCTGAGC 1234  
QY 249 AGTTTCTGAGTGTGACGACACCCCACTGCGCCGAGCGCTTCCGACGAGGCTGCTGT 308  
Db 1235 AGTTTCTGAGTGTGACGACACCCCACTGCGCCGAGCGCTTCCGACGAGGCTGCTGT 1294  
QY 309 GAAAAATACAGAGTGTGAGAGCTTCCAGGCGCATTCATTTCCCGAGCGCAAGGG 368  
Db 1295 GAAAAATACAGAGTGTGAGAGCTTCCAGGCGCATTCATTTCCCGAGCGCAAGGG 1354  
QY 369 CACTGTGTGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCGCGCTGGTACTAC 428  
Db 1355 CACTGTGTGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCGCGCTGGTACTAC 1414  
QY 429 AACCCCTTCAGCGAAACCTGCGCCGCTTTTACTATGTTGTTTACGCGCAACAGAAC 488  
Db 1415 AACCCCTTCAGCGAAACCTGCGCCGCTTTTACTATGTTGTTTACGCGCAACAGAAC 1474  
QY 489 AACTTTGAGCAAGAGCAGTGCCTCGAGTCTTGTGCGGCGCATCTCCAGAGAGGATG 548  
Db 1475 AACTTTGAGCAAGAGCAGTGCCTCGAGTCTTGTGCGGCGCATCTCCAGAGAGGATG 1534  
QY 549 TTTGGCTGAGGGGGAAATPCCCATTTCCAGACACAGGCTCTGTGGAGATGGCTGTGCGA 608  
Db 1535 TTTGGCTGAGGGGGAAATPCCCATTTCCAGACACAGGCTCTGTGGAGATGGCTGTGCGA 1594  
QY 609 GTCTTCTGCTACTCTGATGTTGGTGTGAGGCTCTTGGGTTACTCTTCTTCAAG 668  
Db 1595 GTCTTCTGCTACTCTGATGTTGGTGTGAGGCTCTTGGGTTACTCTTCTTCAAG 1654  
QY 669 AACACAGAAAGAGCTTCCACGACACACACACACACACACACACACACACACACACCTCC 728  
Db 1655 AACACAGAAAGAGCTTCCACGACACACACACACACACACACACACACACACACACCTCC 1714  
QY 729 ACTGTCTTCCACTACCGAGGACAGGAGCAGTCTGTATACACACAGCAGCGGCGCCCTC 788  
Db 1715 ACTGTCTTCCACTACCGAGGACAGGAGCAGTCTGTATACACACAGCAGCGGCGCCCTC 1774  
QY 789 TGAGCCTGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTGCTTCCAGAGGAGGAGGCG 848  
Db 1775 TGAGCCTGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTGCTTCCAGAGGAGGAGGCG 1834  
QY 849 TGGGCTGGGAAAAACTTTTGAACACAGACTCTTGGCTTTTCCAGGCGCACTGTGCTCA 908  
Db 1835 TGGGCTGGGAAAAACTTTTGAACACAGACTCTTGGCTTTTCCAGGCGCACTGTGCTCA 1894  
QY 909 GAGACAGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCAGCTCTGAGAGAGC 968  
Db 1895 GAGACAGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCAGCTCTGAGAGAGC 1954  
QY 969 TCAAGGTTTGGAGGAGCAGAAACCTTTGGCCAGAGATACACAGCTAGATGGAACCTG 1028  
Db 1955 TCAAGGTTTGGAGGAGCAGAAACCTTTGGCCAGAGATACACAGCTAGATGGAACCTG 2014  
QY 1029 CTTGCAATGAGTGTGGAGAGTGGAGTTTGTCTCTCTGTTCAAGGCTGCTGCTC 1088  
Db 2015 CTTGCAATGAGTGTGGAGAGTGGAGTTTGTCTCTCTGTTCAAGGCTGCTGCTC 2074  
QY 1089 CTACCCCATGGTGTAGAGAGAGTGGGTTGGTGTGACACCTCTGGAGGCGCCCAACCTC 1148  
Db 2075 CTACCCCATGGTGTAGAGAGAGTGGGTTGGTGTGACACCTCTGGAGGCGCCCAACCTC 2134  
QY 1149 GTCTCTCCGAGCTCTCTTCCATGCTGTGCGGCCAGGCTGGGAGGAGACTTCCCTGT 1208

Db 2135 GTCTCTCCGAGCTCTCTTCCATGCTGTGCGGCCAGGCTGGAGAGAGACTTCCCTGT 2194  
QY 1209 GTAGTTTGTGCTGTAAGAGAGTGTCTTTTGTATTTAATGCTGTGCAATGSGTGAAGAG 1268  
Db 2195 GTAGTTTGTGCTGTAAGAGAGTGTCTTTTGTATTTAATGCTGTGCAATGSGTGAAGAG 2254  
QY 1269 GAGGGAAGAGGCTGTTTGGCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1328  
Db 2255 GAGGGAAGAGGCTGTTTGGCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2314  
QY 1329 CTCTGCCCTTGATCAGCCCCCCTTGGCTTAGACAGCAGCAGCAGCAGCAGCAGCAGCAGC 1388  
Db 2315 CTCTGCCCTTGATCAGCCCCCCTTGGCTTAGACAGCAGCAGCAGCAGCAGCAGCAGCAGC 2374  
QY 1389 GCTGATTTCCGAGCGCCCGACCCCAAGGTTCTCCAAATCATCACAGCCAGCCGCCCTC 1448  
Db 2375 GCTGATTTCCGAGCGCCCGACCCCAAGGTTCTCCAAATCATCACAGCCAGCCGCCCTC 2434  
QY 1449 GCGTAAATAAAGTGTGTTGTGAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 1492  
Db 2435 GCGTAAATAAAGTGTGTTGTGAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 2478

RESULT 8

ADA01277

ID ADA01277 standard; cdNA; 2482 BP.

XX AC ADA01277;

XX AC

DT 06-NOV-2003 (first entry)

XX Human PRO polynucleotide #5.

XX Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;

XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;

XX adrenal; lung; colon; breast; prostate; cervix; liver; cancer;

XX microvascular endothelial cell; endothelial cell tube formation;

XX sports-related joint problem; articular cartilage defect; osteoarthritis;

XX rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.

XX Homo sapiens.

XX US2003068779-Al.

XX 10-APR-2003.

XX 16-SEP-2002; 2002US-00245107.

XX 09-MAY-2001; 2001US-0290589P.

XX 29-AUG-2001; 2001WO-US027099.

XX 18-JUL-2002; 2002US-00197942.

XX (GETH ) GENENTECH INC.

XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;

XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;

XX Fong S;

XX WPI; 2003-825484/59.

XX P-PSDB; ADA01278.

XX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for

XX stimulating proliferation of human microvascular endothelial cells, and

XX PRO6018 polypeptide useful for stimulating proliferation of chondrocyte

XX cells.

XX Claim 2; Fig 9; 307pp; English.

XX The invention relates to isolated human PRO polypeptides (secreted and

XX transmembrane polypeptides) and the polynucleotides encoding them. The

XX invention also relates to an antibody which specifically binds to a PRO

XX polypeptide, a method for stimulating the release of tumour necrosis

CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the  
 CC proliferation or differentiation of chondrocyte cells and a method for  
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,  
 CC colon, breast, prostate, rectal, cervical and liver tumours). The  
 CC polynucleotides are useful in molecular biology, including uses as  
 CC hybridisation probes, in chromosome and gene mapping, in generating  
 CC antisense RNA and DNA and in gene therapy. The polynucleotides may also  
 CC be used in preparing PRO polypeptides by recombinant techniques and in  
 CC generating either transgenic animals or knock-out animals which are  
 CC useful in the development and screening of therapeutically useful  
 CC reagents. The PRO polypeptides or antibodies are used in preparing a  
 CC medicament for treating a condition responsive to the polypeptides or  
 CC antibodies, such as tumours, for stimulating and inhibiting proliferation  
 CC of human microvascular endothelial cells, for inducing endothelial cell  
 CC tube formation and for treating sports-related joint problems, articular  
 CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence  
 CC represents a human PRO polynucleotide of the invention.

XX Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

Query Match 97.5%; Score 1458; DB 8; Length 2482;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY	9	CACGAGGAGCAGATCTCAAGAGTTTCCTTATGAGGCTGCTTGGGCAACAGAGAAC	68
DB	995	CCACGAGGAGATCTCAAGAGTTTCCTTATGAGGCTGCTTGGGCAACAGAGAAC	1054
QY	69	TACCTTCGGAGAGAGAGTGCATCTAGCTGTGCGGCTGTGCAAGTGGGCTTTGAGA	128
DB	1055	TACCTTCGGAGAGAGAGTGCATCTAGCTGTGCGGCTGTGCAAGTGGGCTTTGAGA	1114
QY	129	GGCAGCTGTGGGCTCAGGCACTTTCCCGAGGCGCTCCATGAGAAAGGCGCATCCA	188
DB	1115	GGCAGCTGTGGGCTCAGGCACTTTCCCGAGGCGCTCCATGAGAAAGGCGCATCCA	1174
QY	189	GTGCTCTGGCACTGTGAGCACTTCAGCCAGTTCGCTGAGCAATGGCTGTGATCGAC	248
DB	1175	GTGCTCTGGCACTGTGAGCACTTCAGCCAGTTCGCTGAGCAATGGCTGTGATCGAC	1234
QY	249	AGTTTCTCGAGTGTGAGCACTTCGCGAGGCGCTCCGAGGAGGCTGCCTGT	308
DB	1235	AGTTTCTCGAGTGTGAGCACTTCGCGAGGCGCTCCGAGGAGGCTGCCTGT	1294
QY	309	GAAATATACAGAGTGGCTTTGACGAGCTCCAGGCTCCATTTCCCGAGCAAGAGG	368
DB	1295	GAAATATACAGAGTGGCTTTGACGAGCTCCAGGCTCCATTTCCCGAGCAAGAGG	1354
QY	369	CACCTCGTGGACCTCCAGACACAGGACTCTGCAAGAGAGGATCCCGCGTGTACTAC	428
DB	1355	CACCTCGTGGACCTCCAGACACAGGACTCTGCAAGAGAGGATCCCGCGTGTACTAC	1414
QY	429	AACCCCTTCAGGAACTATGCGCGCTTTACCTATGCTGTGTTGATCGGCAACAGAAC	488
DB	1415	AACCCCTTCAGGAACTATGCGCGCTTTACCTATGCTGTGTTGATCGGCAACAGAAC	1474
QY	489	AACCTTTGAGGAGAGCAGCAGTGGCTTCAGTCTTCTCGCGCATCTCCAAAGAGATGTG	548
DB	1475	AACCTTTGAGGAGAGCAGCAGTGGCTTCAGTCTTCTCGCGCATCTCCAAAGAGATGTG	1534
QY	549	TTTGCCCTGAGCGGGAATCCCATTCACGACACAGGCTCTGTGGAGATGGCTGTGCA	608
DB	1535	TTTGCCCTGAGCGGGAATCCCATTCACGACACAGGCTCTGTGGAGATGGCTGTGCA	1594
QY	609	GTGTTCTCTGTGATCTGCAATGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT	668
DB	1595	GTGTTCTCTGTGATCTGCAATGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT	1654
QY	669	AACACAGAGAAGGACTTCCAGGACACCAACCAACCAACCAACCAACCAACCAACCA	728
DB	1655	AACACAGAGAAGGACTTCCAGGACACCAACCAACCAACCAACCAACCAACCAACCA	1714
QY	729	ACTGTCTCCACTACCGAGGACAGGAGCAGCTGTGTTCTATACCAACCAACCAACCA	788

DB	1715	ACTGTCTCCACTACCGAGGACACGAGCAGCTGTCTATTAACACACACACCGGCGCCCTC	1774
QY	789	TGAGCCCTGGGTCTCACCGGCTCTCAGCTGGCCCTGCTTCTGCTTCCAGGGAGAGGCC	848
DB	1775	TGAGCCCTGGGTCTCACCGGCTCTCAGCTGGCCCTGCTTCTGCTTCCAGGGAGAGGCC	1834
QY	849	TGGCTCTGGGAAAAAATTTTGAACCCAGAGCTCTGCTGCTTTTCCAGGGCCCACTGTGCTCA	908
DB	1835	TGGCTCTGGGAAAAAATTTTGAACCCAGAGCTCTGCTGCTTTTCCAGGGCCCACTGTGCTCA	1894
QY	909	GAGACAGGGCTCAGCCCTCTTTGGAGAGTCTCAGCTAAGCTCAGCTCTGAGAAGC	968
DB	1895	GAGACAGGGCTCAGCCCTCTTTGGAGAGTCTCAGCTAAGCTCAGCTCTGAGAAGC	1954
QY	969	TCAAAGGTTTGGAGAGGAGCAGAAACCTTGGGCGCAGAGTACCCAGACTAGATGAGCTG	1028
DB	1955	TCAAAGGTTTGGAGAGGAGCAGAAACCTTGGGCGCAGAGTACCCAGACTAGATGAGCTG	2014
QY	1029	CCTGCATAGGAGTTTGGAGAGTGTGAGTTTGTTCCTCTCTTCAAGCTGCTGTCTC	1088
DB	2015	CCTGCATAGGAGTTTGGAGAGTGTGAGTTTGTTCCTCTCTTCAAGCTGCTGTCTC	2074
QY	1089	CTACCCCATGCTGTAGGAGAGGAGTGGGCTGTGTCAGACCTCTGGAGGCGCCCAACCT	1148
DB	2075	CTACCCCATGCTGTAGGAGAGGAGTGGGCTGTGTCAGACCTCTGGAGGCGCCCAACCT	2134
QY	1149	GTCTCTCCGAGCTCTCTTCCATGCTGTGCGCCAGCGCTGGGAGGAGGCTTCCCTGT	1208
DB	2135	GTCTCTCCGAGCTCTCTTCCATGCTGTGCGCCAGCGCTGGGAGGAGGCTTCCCTGT	2194
QY	1209	GTAGTTTGTCTGTAAAGAGTGTCTTTTCTTTTATTTTAACTGCTGGCATGGGTGAAG	1268
DB	2195	GTAGTTTGTCTGTAAAGAGTGTCTTTTCTTTTATTTTAACTGCTGGCATGGGTGAAG	2254
QY	1269	GAGGGAAGAGGCTGTGTGGCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1328
DB	2255	GAGGGAAGAGGCTGTGTGGCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2314
QY	1329	CTCTGCTTGTATCAGCCCCCAGCTTGGCTTGTAGCCAGCAGCAGCAGCAGCAGCAGC	1388
DB	2315	CTCTGCTTGTATCAGCCCCCAGCTTGGCTTGTAGCCAGCAGCAGCAGCAGCAGCAGC	2374
QY	1389	GCTGCATTCGAGCGCCCGCCAGCTTCTTCAACATCATCAGCCCGCCCGCCACT	1448
DB	2375	GCTGCATTCGAGCGCCCGCCAGCTTCTTCAACATCATCAGCCCGCCCGCCACT	2434
QY	1449	GGGTAAATAAAGTGGTTTGTGAAAAAATAAAAAAAAAAAAAAAAAAAAAA	1492
DB	2435	GGGTAAATAAAGTGGTTTGTGAAAAAATAAAAAAAAAAAAAAAAAAAAAA	2478

RESULT 9  
 ADA43706

ID ADA43706 standard; cDNA; 2482 BP.

XX ADA43706;

XX AC ADA43706;

XX DT 20-NOV-2003 (first entry)

XX Human cDNA encoding secreted/transmembrane polypeptide PRO256.

ss; gene; human; PRO; secreted protein; transmembrane protein;  
 endothelial cell tube formation; chondrocyte cell differentiation;  
 microvascular endothelial cell; tumour; lung tumour; colon tumour;  
 breast tumour; prostate tumour; rectal tumour; kidney tumour;  
 liver tumour; cytostatic; vaccine.

OS Homo sapiens.

XX US2003064474-A1.

XX 03-APR-2003.



XX PF 16-SEP-2002; 2002US-00245859.  
 XX PR 29-AUG-2001; 2001MO-US027099.  
 XX PR 18-JUL-2002; 2002US-00197942.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
 XX PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
 XX PI Fong S;  
 XX WI; 2003-605867/57.  
 XX DR P-PSDB; ADA43707.  
 XX PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or  
 XX PT PRO21383, useful in molecular biology, chromosome and gene mapping, in  
 XX PT generating antisense RNA and DNA, and in gene therapy.  
 XX PS Claim 2; Fig 9; 309pp; English.  
 XX CC The invention relates to an isolated secreted/transmembrane (PRO)  
 CC polypeptide, having at least 80% sequence identity to a sequence selected  
 CC from any one of the 57 amino acid sequences given in specification, or to  
 CC a sequence encoded by a nucleic acid molecule selected from any one of  
 CC the nucleic acids deposited under any of the ATCC accession numbers given  
 CC in specification, or a sequence having at least 80% identity to PRO  
 CC lacking its associated signal peptide, an extracellular domain of PRO  
 CC with or without its associated signal peptide. Also included are vectors,  
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding  
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by  
 CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,  
 CC PRO10275, PRO21027, PRO20933 or PRO34274 polypeptide or its agonist) and  
 CC an oligonucleotide probe derived from any one of the above nucleotide  
 CC sequences. PRO6018 polypeptide is useful for stimulating the  
 CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080  
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of  
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006  
 CC polypeptides are useful for inhibiting the proliferation of human  
 CC microvascular endothelial cells. PRO polypeptides are useful for  
 CC detecting the presence of tumour in a mammal, including tumours of lung,  
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,  
 CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21027, PRO20933 and  
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube  
 CC formation. PRO or the antibody are useful in the preparation of a  
 CC medicament for treating a condition responsive to PRO polypeptide. The  
 CC oligonucleotide probes are useful for isolating genomic and cDNA  
 CC nucleotide sequences, for measuring or detecting the expression of an  
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a  
 CC hybridisation probe, in chromosome and gene mapping, in the generation of  
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and  
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The  
 CC present sequence encodes a PRO protein.  
 XX SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;  
 Query Match 97.5%; Score 1468; DB 8; Length 2482;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 QY 9 CACGAGGAGAGATCGACAGCTTTCGTTATGAGGCTGCTTGGCAACAGACAC 68  
 DB 995 CCCACGAGGAGAGATCGACAGCTTTCGTTATGAGGCTGCTTGGCAACAGACAC 1054  
 QY 69 TACCTTCGGGAAGAGAGATCGATTCATAGCTGTCGGGGGTGTGCAAGGTGGGCTTTGAGA 128  
 DB 1055 TACCTTCGGGAAGAGAGATCGATTCATAGCTGTCGGGGGTGTGCAAGGTGGGCTTTGAGA 1114  
 QY 129 GGCAGCTCTGGGGCTAGGGGACCTTTCGCCAGGGGCCCTTCATGTAAAGGGGCCATCCA 188  
 DB 1115 GGCAGCTCTGGGGCTAGGGGACCTTTCGCCAGGGGCCCTTCATGTAAAGGGGCCATCCA 1174  
 QY 189 GTGTGCTCTGGCACCTGTGACGCCACCACCTTCGGCTGCGCAATGGCTGCTGCATCGAC 248

DB 1175 GTGTGCTCTGGCACCTGTGACGCCACCACCTTCGGCTGCGCAATGGCTGCTGCATCGAC 1234  
 QY 249 AGTTTCTCTGGAGTGTGACGACACCCCTCACTGCGCCGCGACGCTCCGAGAGGCTGCTGT 308  
 DB 1235 AGTTTCTCTGGAGTGTGACGACACCCCTCACTGCGCCGCGACGCTCCGAGAGGCTGCTGT 1294  
 QY 309 GAAAAATACACAGTGGCTTTTGAAGAGCTCCAGCGCATCCATTTTCCCGACGACAAAGG 368  
 DB 1295 GAAAAATACACAGTGGCTTTTGAAGAGCTCCAGCGCATCCATTTTCCCGACGACAAAGG 1354  
 QY 369 CACTGCTGGAGCTCCGACGACGAGCTCTGCAAGAGAGAGCATCCGGGCTGGTACTAC 428  
 DB 1355 CACTGCTGGAGCTCCGACGACGAGCTCTGCAAGAGAGAGCATCCGGGCTGGTACTAC 1414  
 QY 429 AACCCTCTCAGCGAACAACCTGCGCCCGCTTTACTATGTTGGTGTGTTAAGGCAACAGAAC 488  
 DB 1415 AACCCTCTCAGCGAACAACCTGCGCCCGCTTTACTATGTTGGTGTGTTAAGGCAACAGAAC 1474  
 QY 489 AACTTTGAGGAAGAGCAGAGTGGCTTCAGTCTTGTGCGGCACTCCAGAGAGATGG 548  
 DB 1475 AACTTTGAGGAAGAGCAGAGTGGCTTCAGTCTTGTGCGGCACTCCAGAGAGATGG 1534  
 QY 549 TTGSCCTTGAGCGCGGAAATCCCAATCCAGCAGACAGCTCTGTGGAGATGCTGTGCA 608  
 DB 1535 TTGSCCTTGAGCGCGGAAATCCCAATCCAGCAGACAGCTCTGTGGAGATGCTGTGCA 1594  
 QY 609 GTGTTCTCTGTCATCTGATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 668  
 DB 1595 GTGTTCTCTGTCATCTGATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1654  
 QY 669 AACACAGAGGAAGAGCTTCCAGGACACACACACACACACACACACACACACACACACAC 728  
 DB 1655 AACACAGAGGAAGAGCTTCCAGGACACACACACACACACACACACACACACACACACAC 1714  
 QY 729 ACTGTCTCCACTTACCGAGGACACGAGACACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 788  
 DB 1715 ACTGTCTCCACTTACCGAGGACACGAGACACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1774  
 QY 789 TGAGCTCTGGTCTACCGGCTCTACCTGCGGCTGTCTCTGCTGTGCGCAAGGACAGAGCC 848  
 DB 1775 TGAGCTCTGGTCTACCGGCTCTACCTGCGGCTGTCTCTGCTGTGCGCAAGGACAGAGCC 1834  
 QY 849 TGGGCTGGGAAAAAATTTTGGAAACAGAGCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 908  
 DB 1835 TGGGCTGGGAAAAAATTTTGGAAACAGAGCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1894  
 QY 909 GAGACAGGCTCAGACCCCTCTTGGAGAGTCTCAGTAAAGTCACTCTCTGAGAAAGC 968  
 DB 1895 GAGACAGGCTCAGACCCCTCTTGGAGAGTCTCAGTAAAGTCACTCTCTGAGAAAGC 1954  
 QY 969 TCAAAAGTTTGGAGGAGCAGAAAACCTTGGGCGCAGAAAGTACCAGACTAGATGAGACCTG 1028  
 DB 1955 TCAAAAGTTTGGAGGAGCAGAAAACCTTGGGCGCAGAAAGTACCAGACTAGATGAGACCTG 2014  
 QY 1029 CTTGATAGGAGTTTGGAGGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAG 1088  
 DB 2015 CTTGATAGGAGTTTGGAGGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAG 2074  
 QY 1089 CTACCCCATGTTGTAGGAAGAGGAGTGGGGTGTGTCAGACCTCTGGAGGCCCCAACCCCT 1148  
 DB 2075 CTACCCCATGTTGTAGGAAGAGGAGTGGGGTGTGTCAGACCTCTGGAGGCCCCAACCCCT 2134  
 QY 1149 GTCTCTCCGAGCTCTCTTCCATGCTGTGCGCCAGAGGCTGGGAGAAAGAGCTTCCCTGT 1208  
 DB 2135 GTCTCTCCGAGCTCTCTTCCATGCTGTGCGCCAGAGGCTGGGAGAAAGAGCTTCCCTGT 2194  
 QY 1209 GTAGTTTGTCTGTAAGAGTGTCTTTTGTGTTTATTTTATGCTGTGGCATGGGTGAAGAG 1268  
 DB 2195 GTAGTTTGTCTGTAAGAGTGTCTTTTGTGTTTATTTTATGCTGTGGCATGGGTGAAGAG 2254  
 QY 1269 GAGGGGAAGAGGCTGTTTGGCCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1328







QY 369 CACTGCTGACCTGCCAGACAGGACTCTCAAGGAGAGCATCCCGCGCTGTACTAC 428  
 Db 1355 CACTGCTGACCTGCCAGACAGGACTCTCAAGGAGAGCATCCCGCGCTGTACTAC 1414  
 QY 429 AACCCCTTCAGCGAAACATGCGCCCGCTTTTACTATGTTGGTTGTACGGCAACAGAAC 488  
 Db 1415 AACCCCTTCAGCGAAACATGCGCCCGCTTTTACTATGTTGGTTGTATGTCACAAAGAAC 1474  
 QY 489 AACTTTGAGGAGAGAGCAGGAGGCTCTGAGTCTTCTCGGGCATCTCCAGAGAGATGTG 548  
 Db 1475 AACTTTGAGGAGAGAGCAGGAGGCTCTGAGTCTTCTCGGGCATCTCCAGAGAGATGTG 1534  
 QY 549 TTTGGCTTGAGCGGGAATCCCATTCACAGACAGGCTCTGTGGAGATGCTCTGCA 608  
 Db 1535 TTTGGCTTGAGCGGGAATCCCATTCACAGACAGGCTCTGTGGAGATGCTCTGCA 1594  
 QY 609 GGTTCCTGCTCATCTGATTTGGTGTGGTGTAGCCTCTGGTGTACTCTTCTCAAG 668  
 Db 1595 GGTTCCTGCTCATCTGATTTGGTGTGGTGTAGCCTCTGGTGTACTCTTCTCAAG 1654  
 QY 669 AACCCAGAGAAAGGACTTCCAGGACACACACACACACACACACACACACACACAC 728  
 Db 1655 AACCCAGAGAAAGGACTTCCAGGACACACACACACACACACACACACACACACAC 1714  
 QY 729 ACTGTCTCACTACCGAGAGACAGGAGACCTGTGTCTATAACACACACACACACAC 788  
 Db 1715 ACTGTCTCACTACCGAGAGACAGGAGACCTGTGTCTATAACACACACACACACAC 1774  
 QY 789 TGAGCTGGTCTCACCGGCTCTCACCTGGCCCTCTTCTGCTGCTGCTGCTGCTGCTCA 848  
 Db 1775 TGAGCTGGTCTCACCGGCTCTCACCTGGCCCTCTTCTGCTGCTGCTGCTGCTGCTCA 1834  
 QY 849 TGGGCTGGGAAATCTTGGAAACAGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCA 908  
 Db 1835 TGGGCTGGGAAATCTTGGAAACAGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCA 1894  
 QY 909 GAGACCGGCTCAGCGCCCTCTTGGAGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCA 968  
 Db 1895 GAGACCGGCTCAGCGCCCTCTTGGAGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCA 1954  
 QY 969 TCAAGGTTTGGAG 1028  
 Db 1955 TCAAGGTTTGGAG 2014  
 QY 1029 CTTGATAGAGTTTGGAGAGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAG 1088  
 Db 2015 CTTGATAGAGTTTGGAGAGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAG 2074  
 QY 1089 CTACCCCTGCTGCTAGAGAGAGTTGGGTTGCTGAGACCTCTGAGAGGAGAGAGAGAG 1148  
 Db 2075 CTACCCCTGCTGCTAGAGAGAGTTGGGTTGCTGAGACCTCTGAGAGGAGAGAGAGAG 2134  
 QY 1149 GTCTCCCGAGCTCTCTTTCATGCTGTGCGCCAGAGGCTGGAGAGAGAGAGAGAGAG 1208  
 Db 2135 GTCTCCCGAGCTCTCTTTCATGCTGTGCGCCAGAGGCTGGAGAGAGAGAGAGAGAG 2194  
 QY 1209 GTAGTTTGTGCTGAGAGAGTTGCTTGTGTTTATTAATGCTGAGAGAGAGAGAGAG 1268  
 Db 2195 GTAGTTTGTGCTGAGAGAGTTGCTTGTGTTTATTAATGCTGAGAGAGAGAGAGAG 2254  
 QY 1269 GAGGGAGAGAGGCTGTTTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1328  
 Db 2255 GAGGGAGAGAGGCTGTTTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2314  
 QY 1329 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1388  
 Db 2315 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2374  
 QY 1389 GCTGATCTCCGAG 1448  
 Db 2375 GCTGATCTCCGAG 2434

QY 1449 GGCTAATAAAGTGTGTTTGTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1492  
 Db 2435 GGCTAATAAAGTGTGTTTGTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2478  
 RESULT 12  
 ADA01033  
 ID ADA01033 standard; cDNA; 2482 BP.  
 AC ADA01033;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX  
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.  
 KW ss: gene; human; PRO: secreted protein; transmembrane protein;  
 endothelial cell tube formation; chondrocyte cell differentiation;  
 microvascular endothelial cell; tumour; lung tumour; colon tumour;  
 breast tumour; prostate tumour; rectal tumour; kidney tumour;  
 liver tumour; cytostatic; vaccine.  
 OS Homo sapiens.  
 XX  
 PN US2003068780-A1.  
 XX  
 PD 10-APR-2003.  
 XX  
 PF 16-SEP-2002; 2002US-00245143.  
 XX  
 PR 02-AUG-2000; 2000US-0222695P.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-AUG-2001; 2001WO-US027099.  
 PR 18-JUL-2002; 2002US-00197942.  
 XX  
 PA (GETH) GENENTECH INC.  
 XX  
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,  
 Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
 Fong S;  
 XX  
 DR WPI; 2003-625485/59.  
 DR P-PSDB; ADA01034.  
 XX  
 PT Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the  
 preparation of a medicament for treating a condition responsive to PRO  
 polypeptide, and as therapeutic agents e.g. vaccines.  
 XX  
 PS Claim 2; Fig 9; 307pp; English.  
 XX  
 CC The invention relates to an isolated secreted/transmembrane (PRO)  
 polypeptide, having at least 80% sequence identity to a sequence selected  
 from any one of the 57 amino acid sequences given in specification, or to  
 a sequence encoded by a nucleic acid molecule selected from any one of  
 the nucleic acids deposited under any of the ATCC accession numbers given  
 in specification, or a sequence having at least 80% identity to PRO  
 lacking its associated signal peptide, an extracellular domain of PRO  
 with or without its associated signal peptide. Also included are vectors,  
 transformed host cells, anti-PRO antibodies, the nucleic acids encoding  
 PRO, PRO fusion proteins, inducing endothelial cell tube formation (by  
 administering PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000,  
 PRO10275, PRO1207, PRO20933 or PRO34274 polypeptide or its agonist) and  
 an oligonucleotide probe derived from any one of the above nucleotide  
 sequences. PRO6018 polypeptide is useful for stimulating the  
 proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080  
 and PRO21383 polypeptides are useful for stimulating the proliferation of  
 human microvascular endothelial cells. PRO6071, PRO487 and PRO6006  
 polypeptides are useful for inhibiting the proliferation of human  
 microvascular endothelial cells. PRO polypeptides are useful for  
 detecting the presence of tumour in a mammal, including tumours of lung,  
 colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,  
 PRO189, PRO499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and  
 PRO34274 polypeptides are useful for inducing endothelial cell tube  
 formation. PRO or the antibody are useful in the preparation of a

medicament for treating a condition responsive to PRO polypeptide. The oligonucleotide probes are useful for isolating genomic DNA. Nucleotide sequences for measuring or detecting the expression of an associated gene, and as antisense probes. PRO nucleic acid is useful as a hybridisation probe, in chromosome and gene mapping, in the generation of antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The present sequence encodes a PRO protein.

Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

Query Match      97.5%;    Score 1468;    D3 8;    Length 2482;

Query Match: 97.3%; Score 1468; RS 6; Length 2482;  
Best Local Similarity 99.3%; Pred. No. 0;

Best Local Similarity 99.58; Freq. NO: 0;  
Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 9 CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAAGAACAC 68

db 995 CCCACGGAGCAGATCTGCAAGAGTTTCGTTATGGAGGCTGCTTGGGCAACAAGAACAC 1054

QY 69 TACCTTCGGGAAGAAGAGTGCAATCTAGCCCTGTGGGGTGTGCAAGGTGGCCCTTGAGA 128

db 1055 TACCTTCGGGAAGAAGAGTGCAATTCTAGCCCTGTCCGGGTGTGCAGGTGGCCCTTGAGA 1114

QY 129 GGCAGCTCTGGGGCTCAGGCGACTTCCCCCAGGGCCCCCTCCATGGAAGCGGCCATCCA 188

db 1115 GGCAGCTCTGGGGCTCAGGCGACTTTCCTCCCGAGGGCCCTTCCATGGAAAGGGCGCATCCA 11174

OV 189 GTGTGCTCTGGCACTGTTCAGACCACTTCGGTGTGTCATCGAC 248

1175 GTGTGTCCTGGCACCTGTGAGGCCACCGCATTTCCGCTGCAGCAATGGCTGCTGCATCGAC 1234

249 AGTTTCCTGGAGTGTGACGACACCCGCCAATGCCCCCGGCGGTCGCGTGGT 308

1235 1234

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Year	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
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Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

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[illegible][illegible][illegible][illegible]

DD 1775 TGAAGCCCTGGGATCTCATCCCTGGCCCCCTGCCTTTCCTGCCTTGACAGGCGCAGAGGCC 1834

PR 02-JUN-2000; 2000HO-US015264.  
PR 28-AUG-2001; 2001HO-US027099.  
XX 18-JUL-2002; 2002US-00197942.  
PA (GETH ) GENENTECH INC.  
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,  
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
PI Pong S;  
XX WPI; 2003-585304/55.  
DR P-PSDB; ADA43591.  
XX  
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or  
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in  
PT generating antisense RNA and DNA, and in gene therapy.  
XX  
PS Claim 2; Fig 9; 352pp; English.  
XX  
CC The invention relates to an isolated secreted/transmembrane (PRO)  
CC polypeptide, having at least 80% sequence identity to a sequence selected  
CC from any one of the 57 amino acid sequences given in specification, or to  
CC a sequence encoded by a nucleic acid molecule selected from any one of  
CC the nucleic acids deposited under any of the ATCC accession numbers given  
CC in specification, or a sequence having at least 80% identity to PRO  
CC lacking its associated signal peptide, an extracellular domain of PRO  
CC with or without its associated signal peptide. Also included are vectors,  
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding  
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by  
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,  
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and  
CC an oligonucleotide probe derived from any one of the above nucleotide  
CC sequences. PRO6018 polypeptide is useful for stimulating the  
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080  
CC and PRO21383 polypeptides are useful for stimulating the proliferation of  
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006  
CC polypeptides are useful for inhibiting the proliferation of human  
CC microvascular endothelial cells. PRO polypeptides are useful for  
CC detecting the presence of tumour in a mammal, including tumours of lung,  
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,  
CC PRO189, PRO4499, PRO6308, PRO10275, PRO21207, PRO20933 and  
CC PRO34274 polypeptides are useful for inducing endothelial cell tube  
CC formation. PRO or the antibody are useful in the preparation of a  
CC medicament for treating a condition responsive to PRO polypeptide. The  
CC oligonucleotide probes are useful for isolating genomic and cDNA  
CC nucleotide sequences, for measuring or detecting the expression of an  
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a  
CC hybridisation probe, in chromosome and gene mapping, in the generation of  
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and  
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The  
XX present sequence encodes a PRO protein.  
SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

QY 249 AGTTTCCTGGAGTGTGACGACACCCCAACGCGCTCCGACGAGGCTGCTGT 308  
DB 1235 AGTTTCCTGGAGTGTGACGACACCCCAACGCGCTCCGACGAGGCTGCTGT 1294  
QY 309 GAAATAACAGAGTGGCTTTGACGAGCTCCAGGCGATCCATTTCCCGAGGACGAGG 368  
DB 1295 GAAATAACAGAGTGGCTTTGACGAGCTCCAGGCGATCCATTTCCCGAGGACGAGG 1354  
QY 369 CACTGCGTGGACCTGCGCAGACACAGGACTCTGCGAAGGAGAGCATCCCGGCTGGTACTAC 428  
DB 1355 CACTGCGTGGACCTGCGCAGACACAGGACTCTGCGAAGGAGAGCATCCCGGCTGGTACTAC 1414  
QY 429 AACCCCTTCAGCGAACACTGCGCGCGCTTTACCTATGCTGTGTTTACGCGAACAGAAC 488  
DB 1415 AACCCCTTCAGCGAACACTGCGCGCGCTTTACCTATGCTGTGTTTATGGCAACAGAAC 1474  
QY 489 AACTTTGAGGAAGAGCAGCAGTGGCTGCTGAGTCTTGTGCGGCGCATCTCCAAGAGGATGTG 548  
DB 1475 AACTTTGAGGAAGAGCAGCAGTGGCTGCTGAGTCTTGTGCGGCGCATCTCCAAGAGGATGTG 1534  
QY 549 TTGCGCTTGAGCGCGGGAATCCCATTTCCAGCAGCAGGCTCTGTGGAGATGGCTGTGCGA 608  
DB 1535 TTGCGCTTGAGCGCGGGAATCCCATTTCCAGCAGCAGGCTCTGTGGAGATGGCTGTGCGA 1594  
QY 609 GTGTTCTGCTCATCTGCTGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 668  
DB 1595 GTGTTCTGCTCATCTGCTGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1654  
QY 669 AACCAAGAAAGGACTTCCACGCGACACCAACCAACCAACCAACCAACCAACCAACCAACCA 728  
DB 1655 AACCAAGAAAGGACTTCCACGCGACACCAACCAACCAACCAACCAACCAACCAACCAACCA 1714  
QY 729 ACTGCTCCACTACCGAGGACACCGAGCAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 788  
DB 1715 ACTGCTCCACTACCGAGGACACCGAGCAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1774  
QY 789 TGAGCGTGGTCTCACCGGCTCTCACCTGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 848  
DB 1775 TGAGCGTGGTCTCACCGGCTCTCACCTGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1834  
QY 849 TGGGCTGGGAAAGGACTTTGGAACAGCAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 908  
DB 1835 TGGGCTGGGAAAGGACTTTGGAACAGCAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 1894  
QY 909 GAGACACGAGGCTCCAGCGCTCTTTGGAGAGTCTCAGCTAAGCTCAGCTCTGAGAGAGC 968  
DB 1895 GAGACACGAGGCTCCAGCGCTCTTTGGAGAGTCTCAGCTAAGCTCAGCTCTGAGAGAGC 1954  
QY 969 TCAAGGTTTGGAGAGGACGAGAAACCTTGGGCGAGAGTACAGACTAGATGAGACCTG 1028  
DB 1955 TCAAGGTTTGGAGAGGACGAGAAACCTTGGGCGAGAGTACAGACTAGATGAGACCTG 2014  
QY 1029 CCTGCATAGGAGTTTGGAGAGGAGTTGGAGTTTGGTTTCTCTGTTTCAAGCTGCTGTGCC 1088  
DB 2015 CCTGCATAGGAGTTTGGAGAGGAGTTGGAGTTTGGTTTCTCTGTTTCAAGCTGCTGTGCC 2074  
QY 1089 CTACCCCATGCTGTGAGAGAGAGTGGGTGGGTGAGTGTGAGACCTTGGAGGCGCCCAACCT 1148  
DB 2075 CTACCCCATGCTGTGAGAGAGAGTGGGTGGGTGAGTGTGAGACCTTGGAGGCGCCCAACCT 2134  
QY 1149 GTCTCTCCGAGCTCTCTTCCATGCTGTGCGCGCAGGCTGGGAGGAGGAGCTTCCCTGT 1208  
DB 2135 GTCTCTCCGAGCTCTCTTCCATGCTGTGCGCGCAGGCTGGGAGGAGGAGCTTCCCTGT 2194  
QY 1209 GTAGTTTGTGCTGTAAGAGAGTGTCTTTTGTGTTTAAATGCTGTGCTGCTGGTGAAGAG 1268  
DB 2195 GTAGTTTGTGCTGTAAGAGAGTGTCTTTTGTGTTTAAATGCTGTGCTGCTGGTGAAGAG 2254  
QY 1269 GAGGAGAGAGGCTGTGTTGGCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1328  
DB 2255 GAGGAGAGAGGCTGTGTTGGCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2314







Qy	69	TACCTTCGGGAGAGAGTGCATTCTAGCTGTGCGGGTGTGCAAGGTGGGCTTTTGAGA	128
Db	1055	TACCTTCGGGAGAGAGTGCATTCTAGCTGTGCGGGTGTGCAAGGTGGGCTTTTGAGA	1114
Qy	129	GGCAGCTCTGGGCTCAGCGACTTTCCCGCAGGGCCCTCCATGGAAGGGGCCATCCA	188
Db	1115	GGCAGCTCTGGGCTCAGCGACTTTCCCGCAGGGCCCTCCATGGAAGGGGCCATCCA	1174
Qy	189	GTGTCTCTGGCAGCTCTGAGCCACCCAGATTCGCGCTGAGCAATGGCTGTGATCGAC	248
Db	1175	GTGTCTCTGGCAGCTCTGAGCCACCCAGATTCGCGCTGAGCAATGGCTGTGATCGAC	1234
Qy	249	AGTTTCTGAGGTGAGCAGACCCGCCAACTGCGCCCGGACGCTCCGACGAGGCTGCTGT	308
Db	1235	AGTTTCTGAGGTGAGCAGACCCGCCAACTGCGCCCGGACGCTCCGACGAGGCTGCTGT	1294
Qy	309	GAAATATACAGAGTGGCTTTGACAGCTCCAGCGCATCCATTTCCCGCAGCGACAAAGGG	368
Db	1295	GAAATATACAGAGTGGCTTTGACAGCTCCAGCGCATCCATTTCCCGCAGCGACAAAGGG	1354
Qy	369	CACTCGGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGGCTGTGACTAC	428
Db	1355	CACTCGGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGGCTGTGACTAC	1414
Qy	429	AACCCCTTCAGGAACTGCGCCCGCTTTACCTATGGTGTGTTAGCGCAACAGAAC	488
Db	1415	AACCCCTTCAGGAACTGCGCCCGCTTTACCTATGGTGTGTTAGCGCAACAGAAC	1474
Qy	489	AACTTTGAGGAAGAGCAGTGCCTCGAGTCTTGTGCGGCATCTCCAAGAGGANGTG	548
Db	1475	AACTTTGAGGAAGAGCAGTGCCTCGAGTCTTGTGCGGCATCTCCAAGAGGANGTG	1534
Qy	549	TTTGGCTGAGCGGGAAATCCCATTCACAGCAGGCTCTGAGAGTGGCTGTGCA	608
Db	1535	TTTGGCTGAGCGGGAAATCCCATTCACAGCAGGCTCTGAGAGTGGCTGTGCA	1594
Qy	609	GTGTTCTCGTCACTGCACTGTGCTGTGGTGTAGCCATCTTGGGTACTGCTTTCAAG	668
Db	1595	GTGTTCTCGTCACTGCACTGTGCTGTGGTGTAGCCATCTTGGGTACTGCTTTCAAG	1654
Qy	669	AACCAAGAAAGACTTCCAGGACACACACACACACACACACACACACACACACAC	728
Db	1655	AACCAAGAAAGACTTCCAGGACACACACACACACACACACACACACACACACAC	1714
Qy	729	ACTGCTCCACTACAGAGACACGAGCAGCTGTGCTATTAACCAACACACACACAC	788
Db	1715	ACTGCTCCACTACAGAGACACGAGCAGCTGTGCTATTAACCAACACACACACAC	1774
Qy	789	TGAGCTGGGTCTCACCGGCTCTACCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT	848
Db	1775	TGAGCTGGGTCTCACCGGCTCTACCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT	1834
Qy	849	TGGGCTGGGAAATCTTTGGAACACAGACTCTTGGCTGCTGCTGCTGCTGCTGCTCA	908
Db	1835	TGGGCTGGGAAATCTTTGGAACACAGACTCTTGGCTGCTGCTGCTGCTGCTGCTCA	1894
Qy	909	GAGCCAGGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCAGCTCTGAGAAAGC	968
Db	1895	GAGCCAGGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCAGCTCTGAGAAAGC	1954
Qy	969	TCAAGGTTTGAAGAGCGAAGAACCTTGGCGCAGAGTACAGAGTACAGTGGACCTG	1028
Db	1955	TCAAGGTTTGAAGAGCGAAGAACCTTGGCGCAGAGTACAGAGTACAGTGGACCTG	2014
Qy	1029	CCTGCATAGGAGTTTGGAGAGTTGGAGTTTGTCTCTGTTTCAAGCTGCTGTCC	1088
Db	2015	CCTGCATAGGAGTTTGGAGAGTTGGAGTTTGTCTCTGTTTCAAGCTGCTGTCC	2074
Qy	1089	CTACCCCATGTGCTAGGAAGAGAGTGGGTTGGTGTGAGACCTTGGAGGCCCCCAACCT	1148
Db	2075	CTACCCCATGTGCTAGGAAGAGAGTGGGTTGGTGTGAGACCTTGGAGGCCCCCAACCT	2134

Search completed: April 22, 2004, 05:19:43  
Job time : 645 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 22, 2004, 02:57:27 ; Search time 6021 Seconds  
(without alignments)  
10833.959 Million cell updates/sec

Title: US-09-935-390A-4  
Perfect score: 1505  
Sequence: 1 GAATTCGCACGAGCAGCAG.....AAAAAAGTCCTCGGGCGGC 1505

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

1: gb.ba.\*

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32: em.htg.other.\*

33: em.htg.mus.\*

34: em.htg.pin.\*

35: em.htg.rod.\*

36: em.htg.man.\*

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39: em.htgo.hum.\*

40: em.htgo.mus.\*

41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1505	100.0	1505	6	BD063229	Secreted
2	1468	97.5	2482	6	AX077023	Sequence
3	1468	97.5	2482	6	AX201332	Sequence
4	1468	97.5	2482	6	AX211596	Sequence
5	1468	97.5	2482	6	AX454456	Sequence
6	1468	97.5	2482	6	AX490934	Sequence
7	1468	97.5	2482	6	AX574482	Sequence
8	1468	97.5	2482	9	AY358969	Homo sapi
9	1460	97.0	2370	9	AY296715	Homo sapi
10	1458.6	96.9	1870	6	AR123705	Sequence
11	1458.6	96.9	1870	6	BD205506	Human pro
12	1363.6	90.6	2297	9	BC004140	Homo sapi
13	1363.6	90.6	2297	9	BC004140	Homo sapi
14	1344.6	89.3	2399	9	AB000095	Homo sapi
15	1013.8	67.4	1037	6	AX067320	Sequence
16	832.8	59.3	178248	9	AC012476	Homo sapi
17	886.4	58.9	115793	9	AC025166	Homo sapi
18	667.4	44.3	1542	6	AR148260	Sequence
19	667.4	44.3	1542	6	E12898	Human cDNA
20	667.4	44.3	1542	6	E21838	Preventive
21	667.4	44.3	1542	6	AR237449	Sequence
22	665.4	44.2	1542	9	BT007425	Homo sapi
23	665.4	44.2	1542	12	BT009882	Sequence
24	620.8	41.2	127953	2	AC022835	Synthetic
25	552.6	36.7	2173	10	BC005769	Homo sapi
26	550.8	36.6	81200	2	AC022086	Mus muscu
27	550.6	36.6	2228	10	AF099018	Homo sapi
28	522.2	34.7	2534	10	BC053341	Mus muscu
29	419.4	27.9	542	6	AX261151	Sequence
30	413.4	27.5	816	6	BD241927	Compounds
31	413.4	27.5	816	6	AR237110	Sequence
32	413.4	27.5	816	6	AR260603	Sequence
33	413.4	27.5	816	6	AR278134	Sequence
34	413.4	27.5	816	6	AR366830	Sequence
35	413.4	27.5	816	6	AR370726	Sequence
36	413.4	27.5	816	6	AR392231	Sequence
37	413.4	27.5	816	6	AR399866	Sequence
38	413.4	27.5	816	6	AR405133	Sequence
39	413.4	27.5	816	6	AX106233	Sequence
40	413.4	27.5	816	6	AX140524	Sequence
41	413.4	27.5	816	6	AX200384	Sequence
42	413.4	27.5	816	6	AX267040	Sequence
43	413.4	27.5	816	6	BD070163	Compounds
44	378.6	25.2	388	6	AX396029	Sequence
45	357.8	23.8	760	6	BD241950	Compounds

## ALIGNMENTS

RESULT	1	1505 bp	DNA	linear	PAT 27-AUG-2002
BD063229	BD063229	Secreted human proteins.			
LOCUS	Secreted				
DEFINITION	BD063229				
ACCESSION	BD063229				
VERSION	BD063229.1	GI:22608832			
KEYWORDS	JP 2001505783-A/4.				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 1505)				
AUTHORS	Escobedo, J., Hu, Q., Garcia, P., Williams, L.T. and Kothakota, S.				
TITLE	Secreted human proteins				
JOURNAL	Patent: JP 2001505783-A 4 08-MAY-2001;				
	CHIRON CORP				

PN	JP	2001505783--A/4
PD	08-MAY-2001	
PF	11-DEC-1997	JP 1998526977
PR	11-DEC-1996	US 60/032757
PI	JAI ME ESCOBEDO, QUIJANIN HU, PABLO GARCIA, LEWIS T WILLIAMS PI	
	SRINIVAS KOTHAKOTA	
PC	C12N15/12, C12N15/52, C12N15/85, C12N5/10, C12N1/21, C07K14/47, PC	
	C07K16/18	
CC	Strandedness: Single;	
CC	Topology: Linear;	
PH	Key	Location/Qualifiers.
FEATURES	Location/Qualifiers	
source	1..1505	
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	/mol_type="genomic DNA"	
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ORIGIN		
	Query Match	100.0%; Score 1505; DB 6; Length 1505;
	Best local Similarity	100.0%; Pred. No. 0;
	Matches 1505; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	GAATTCGGACGAGGAGAGATCTGCAAGATTTCTGTTATGAGAGGCTGCTTGGGCAACA 60
Dd	1	GAATTCGGACGAGGAGAGATCTGCAAGATTTCTGTTATGAGAGGCTGCTTGGGCAACA 60
Qy	61	AGACAACTACTCTTGGGAGAGAGATGTCATTTCTAGCTGTGCGGCTGTGCAAGTGCGGC 120
Dd	61	AGACAACTACTCTTGGGAGAGAGATGTCATTTCTAGCTGTGCGGCTGTGCAAGTGCGGC 120
Qy	121	CTTTGAGAGGAGCTCTGGGGCTCAGGCGACTTTTCCCGAGGGGCCCTTCCATGGAAGGC 180
Dd	121	CTTTGAGAGGAGCTCTGGGGCTCAGGCGACTTTTCCCGAGGGGCCCTTCCATGGAAGGC 180
Qy	181	GCCATCCAGTGTCTTGGCACTGTGTAGCCACCCAGTTCCGCTGAGCGAATGCTGCT 240
Dd	181	GCCATCCAGTGTCTTGGCACTGTGTAGCCACCCAGTTCCGCTGAGCGAATGCTGCT 240
Qy	241	GCATCGACAGTTTCTCGAGTGTGACGACACCCCCCACTGCCCGAGCCCTCCGACGAGG 300
Dd	241	GCATCGACAGTTTCTCGAGTGTGACGACACCCCCCACTGCCCGAGCCCTCCGACGAGG 300
Qy	301	CTGCCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGGCATTCATTTCGCCAGG 360
Dd	301	CTGCCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGGCATTCATTTCGCCAGG 360
Qy	361	ACAAAGGCACTGGCTGACCTGTCAGACACAGGACTCTGCAAGAGAGACATCCCGCGCT 420
Dd	361	ACAAAGGCACTGGCTGACCTGTCAGACACAGGACTCTGCAAGAGAGACATCCCGCGCT 420
Qy	421	GGTACTACAAACCCCTTTCAGCGAAACATGCGCCGCTTTTACCTATGCTGGTTGTTACGGCA 480
Dd	421	GGTACTACAAACCCCTTTCAGCGAAACATGCGCCGCTTTTACCTATGCTGGTTGTTACGGCA 480
Qy	481	ACAAGAACAACTTTGAGGAGAGAGAGAGTGGCTCGAGTCTTGTGCGGCATCTCCAGA 540
Dd	481	ACAAGAACAACTTTGAGGAGAGAGAGAGTGGCTCGAGTCTTGTGCGGCATCTCCAGA 540
Qy	541	AGGATGTTGTTGGCTGTAGGCGGGAAATCCCAATTCACAGCAGAGCTCTGTGGAGATGG 600
Dd	541	AGGATGTTGTTGGCTGTAGGCGGGAAATCCCAATTCACAGCAGAGCTCTGTGGAGATGG 600
Qy	601	CTGTCCGAGTGTCTTGTTGTCATCTGCAATGTGGTGTGTAGCCATCTTGGGTTACTGCT 660
Dd	601	CTGTCCGAGTGTCTTGTTGTCATCTGCAATGTGGTGTGTAGCCATCTTGGGTTACTGCT 660
Qy	661	TCTTCAAGAACACGAGAGAGGACTTCCAGGACACCCACACACACCCACCCACCCCTG 720
Dd	661	TCTTCAAGAACACGAGAGAGGACTTCCAGGACACCCACACACACCCACCCACCCCTG 720
Qy	721	CCAGCTCCACTGTCTTCCATACCGGAGACCGGAGCAGCTGTATATACCAACCAACGC 780
Dd	721	CCAGCTCCACTGTCTTCCATACCGGAGACCGGAGCAGCTGTATATACCAACCAACGC 780



Db 1055 TACCTTCGGGAAGAAGAGTGCATTTCTAGCTGTGCGGGTGTGCAAGTGGGCTTTTGAGA 1114  
Qy 129 GGCAGCTCTGGGGCTCAGGGCGATTCTTCCCGCCAGGGCCCTCCATGGAAGAGCGCCCATCCA 188  
Db 1115 GGCAGCTCTGGGGCTCAGGGCGATTCTTCCCGCCAGGGCCCTCCATGGAAGAGCGCCCATCCA 1174  
Qy 189 GTGTGCTCTGGCACTGTGAGCCCAAGCCAGTTCGGTGGAGCAATGGCTGCTGCATCGAC 248  
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Qy 309 GAAAAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCATTCCCGAGCGCAAGGG 368  
Db 1295 GAAAAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCATTCCCGAGCGCAAGGG 1354  
Qy 369 CACTGCGTGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC 428  
Db 1355 CACTGCGTGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC 1414  
Qy 429 AACCCCTTCAGCGAACTCTGGCGCGCTTTTACTATGGTGGTGTGACGCAACAGAAAC 488  
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REFERENCE  
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Gurney A.L., Kirchhofer D.K. and Wood W.I.  
Inhibitor of hepatocyte growth factor activator for use in  
modulation of angiogenesis and cardiovascularization  
Patent: WO 0159100-A 1 16-AUG-2001;  
Genentech, Inc. (US)  
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	Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,		
	Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,		
	Paoni, N.P., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.		
	and Ye, W.		
TITLE	Compositions and methods for the diagnosis and treatment of		
	disorders involving angiogenesis		
JOURNAL	Patent: WO 0208284-A 41 31-JAN-2002;		
	Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone		
	(US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard,		
	Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US);		
	Hillan, Kenneth J. (US); Marsters, Scot A. (US); Pan, James (US)		
	; Paoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US);		
	Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William		
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VERSION AX490934.1 GI:22323804  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.B., Goddard,A.,  
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,  
Pavoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.  
and Ye,W.  
TITLE Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
JOURNAL Patent: WO 0200690-A 41 03-JAN-2002;  
Genentech, Inc. (US)  
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Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,  
Goddard, A., Wood, W.I., and Godowski, P.  
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
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A Bioinformatics Assessment  
Genome Res. 13 (10), 2265-2270 (2003)  
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2 (bases 1 to 2482)  
Clark, H.F.  
Direct Submission  
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Hillman, J.L., Tang, T.Y., Lal, P., Corley, N.C., Guegler, K.J. and  
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PF 28-APR-1999 JP 2000547229  
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PI JENNIFER L HILLMAN, TOM Y TANG, PREETI LAL, NEIL C CORLEY, KARL J  
GUEGLER,  
PI CHANDRA PATTERSON

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ORGANISM Homo sapiens  
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AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
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Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smal, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A., 2001  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 MEDLINE 22388257  
 PUBMED 12477932  
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 AUTHORS Strausberg R.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-DEC-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 COMMENT Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed By: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing By: Genome Sequence Centre,  
 BC Cancer Agency, Vancouver, BC, Canada  
[info@bcgsc.bc.ca](mailto:info@bcgsc.bc.ca)  
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,  
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,  
 Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo  
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 Schein, Duane Smalius, Michael Smith, Lorraine Spence, Jeff Stott,  
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REFERENCE 1 (sites)
AUTHORS Shimomura,T., Denda,K., Kitamura,A., Kawaguchi,T., Kito,M.,
Kondo,J., Kagaya,S., Qin,L., Takata,H., Miyazawa,K. and Kitamura,N.
TITLE Hepatocyte growth factor activator inhibitor, a novel Kunitz-type
serine protease inhibitor
J. Biol. Chem. 272 (10), 6370-6376 (1997)
JOURNAL 97197808
MEDLINE 9045658
PUBMED 9045658
REFERENCE 2 (bases 1 to 2399)
AUTHORS Denda,K.
TITLE Direct Submission
JOURNAL Submitted (24-DEC-1996) Kimitoshi Denda, Tokyo Institute of
Technology, Department of Life Science, 4259 Nagatsuta, Midori-ku,
Yokohama, Kanagawa 227, Japan (E-mail:kdenda@bio.titech.ac.jp,
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TRRL"
polyA_signal
2379..2384
ORIGIN
Query Match 89.1%; Score 1344.6; DB 9; Length 2399;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 1408; Conservative 0; Mismatches 9; Indels 48; Gaps 1;
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Search completed: April 22, 2004, 07:00:18  
Job time : 6031 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 22, 2004, 08:10:04 ; Search time 2501 Seconds  
(without alignments)  
2459.660 Million cell updates/sec

Title: US-09-935-390A-23  
Perfect score: 1167  
Sequence: 1 MERRHVCVSGTCQTOFRCS.....TVSTTDETHLVNHTREL 206

Scoring table:  
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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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Database :

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- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
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- 7: em\_estro:\*
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- 9: gb\_estl:\*
- 10: gb\_est2:\*
- 11: gb\_hic:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: gb\_estfun:\*
- 16: em\_estom:\*
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- 23: em\_gss\_man:\*
- 24: em\_gss\_mus:\*
- 25: em\_gss\_pro:\*
- 26: em\_gss\_rod:\*
- 27: em\_gss\_phg:\*
- 28: em\_gss\_vr1:\*

29: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	1167	100.0	1183	9	AL558524	AL558524 AL558524
3	1164	99.7	1004	13	BX360990	BX360990 BX360990
4	1156	99.1	1201	13	BX388310	BX388310 BX388310
5	1154	98.9	635	12	BM820520	BM820520 K-EST0089
6	1141	97.8	862	14	CA488310	CA488310 AGENCOURT
7	1074.5	92.1	973	14	CA488377	CA488377 AGENCOURT
8	1063.5	91.1	925	12	BG291726	BG291726 602388738
9	1031	88.3	663	12	BG697670	BG697670 602660928
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17	885.5	75.9	890	12	BG746579	BG746579 602703881
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22	846	72.5	740	10	BE740145	BE740145 601595087
23	842	72.2	563	11	BC020485	BC020485 Mus muscu
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27	832.5	71.3	816	12	B1910513	B1910513 603067895
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32	796	68.2	1336	29	AY418946	AY418946 Homo sapi
33	796	68.2	611	12	EN008657	EN008657 603618324
34	784	67.2	411	12	BM844926	BM844926 K-EST0123
35	784	67.2	775	12	BG387116	BG387116 602455829
36	780	66.8	592	12	B1346114	B1346114 375143 MA
37	768.5	65.9	458	10	B8615990	B8615990 601441583
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ALIGNMENTS

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ACCESSION BQ687222  
VERSION BQ687222.1 GI:21812538  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 888)





Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1201)  
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7854.f For more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CSIAI002Z806QPI&cluster=7854.f. Contact :  
Feng liang Email: fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
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## FEATURES

source

## ORIGIN

## Alignment Scores:

Pred. No.: 3,34e-108 Length: 1201  
Score: 1156.00 Matches: 204  
Percent Similarity: 99.51% Conservative: 0  
Best Local Similarity: 99.51% Mismatches: 1  
Query Match: 99.06% Indels: 0  
DB: 13 Gaps: 0

US-09-935-390A-23 (1-206) x BX385810 (1-1201)

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QY 21 AsnGlyCysValleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40  
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QY 61 PheProSerAspLysGlyHisCysValleAspLeuProAspThrGlyLeuCysLysGluSer 80  
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QY 161 GLYThrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisProPro 180  
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QY 201 HisThrThrArgPro 205  
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## RESULT 5

EM820520

LOCUS

DEFINITION

K-EST0089070 S20T665307 Homo sapiens cDNA clone S20T665307-7-H10

5', mRNA sequence.

ACCESSION

EM820520

VERSION

EM820520.1

GI:19176933

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 635)

AUTHORS

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

Oh,K.J., Cheong,J.S., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

Kim,Y.S.

TITLE

21C Frontier Korean EST Project 2001

JOURNAL

Unpublished (2002)

COMMENT

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience &amp; Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 7 row: H column: 10

High quality sequence stop: 635.

FEATURES

Location/Qualifiers

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/notes="Organ: Stomach; Vector: pCNS; Site: 1: EcoRI;

Site 2: NotI; The poly (A) + RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then decapped

with tobacco acid pyrophosphatase (TAP). The decapped

intact mRNA was ligated with DNA-RNA linker including EcoR

I site by treatment of T4 RNA ligase and the first strand

cDNA was synthesized from oligo dt-selected mRNA by

priming with dt-tailed vector. The dt-tailed vector was

adjusted to have about 60nt. The cDNA vector was

circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transformation of

competent cells E. coli Top10F by electroporation method.

The cDNA libraries constructed by this method are

full-length enriched cDNA library."

## ORIGIN

## Alignment Scores:

Pred. No.: 2.2e-108 Length: 635  
Score: 1154.00 Matches: 206  
Percent Similarity: 99.52% Conservative: 0  
Best Local Similarity: 99.52% Mismatches: 0  
Query Match: 98.89% Indels: 1

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Db	135	TCCGACGAGCTGCTGTGAAAATACACAGTGTCTTTCACGAGTCCAGCCGATCCAT	194
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QY	180	roProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyra	200
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Directionally cloned. Priming method: oligo-dT. Average			
insert size: 1800 bp. Library amplification: 26,000 fold.			
Kristi A. Eglund, James J. Vincent, Robert Strausberg,			
Bungkook Lee & Ira Pastan: Discovery of new breast			
cancer genes encoding membrane and secreted proteins.			
Manuscript submitted."			
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QY	180	roProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyra	200
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VERSION	EST.		
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ORGANISM	Homo sapiens		
REFERENCE	1	(bases 1 to 973)	
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaabs-remail.nih.gov Tissue Procurement: Kristi A. Eglund, Ira Pastan CDNA Library Preparation: Invitrogen Corp CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: ILAM14279 row: c column: 13 High quality sequence stop: 598.		
FEATURES	source		
	1..973	Location/Qualifiers	
	/organism="Homo sapiens"		
	/mol_type="mrna"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:6720133"		
	/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hERT-HMEL, LNCap"		
	/lab_host="EMD108"		
	/clone_lib="MASC1"		
	/notes="vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I; Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Eglund, James J. Vincent, Robert Strausberg, Bungkook Lee & Ira Pastan. Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."		
ORIGIN			
Alignment Scores:	Length:	973	
Pred. No.:	6.12e-100	Matches:	195
Score:	1074.50	Conservative:	0
Percent Similarity:	96.06%	Mismatches:	6
Best local Similarity:	96.06%	Indels:	2
Query Match:	92.07%	Gaps:	1
DB:	14		
US-09-935-390A-23	(1-206) x CA488377	(1-973)	
QY	6	ProValCysSerGlyThrCysGlnProThrGlnPheArgCysSerAsnGlyCysCysile	25
DB	184	CCAGTGTCCTTGGACCTCTGAGCCACCCAGTTCGGCTGCGAGCAATGGCTGTCATC	243
QY	26	AspSerPheLeuGluCysAspAspThrProAsnCysProAspAlaSerAspGluAla	45
DB	244	GACAGTTTCTCGAGTGTGACGACACCCCACTGCCCGAGCCTCCGACGAGGCTGCC	303
QY	46	CysGlnLysThrSerGlyPheAspGluGlnArgLleHisPheProSerAspLys	65
DB	304	TGTGAAATAACACAGTGGCTTTGACAGCTTCGAGGATTCATTTCCCGAGTGCACA	363

## Alignment Scores:

Pred. No.: 7,74e-99 Length: 925  
 Score: 1063.50 Matches: 198  
 Percent Similarity: 96.12% Conservatives: 0  
 Best Local Similarity: 96.12% Mismatches: 7  
 Query Match: 91.13% Indels: 3  
 DB: 12 Gaps: 1

US-09-935-390A-23 (1-206) x BG291726 (1-925)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
 Db 33 ATGGAAGGCGCCATCCAGTGTCTGCGACCTGTGAGCCACCACGATTCGCTGCAGC 92  
 QY 21 AsnGlyCysCysLeuAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40  
 Db 93 AATGGCTGTGTCATCGACAGTTCCTGAGTGTGACGACACCCCACTGCCCCGAGCC 152  
 QY 41 SerAspGluAlaAlaCysGluValThrSerGlyPheAspGluLeuGlnArgHis 60  
 Db 153 TCGACGAGCTGCTGTGAAATACAGAGTGTTCAGAGCTCCAGCATTCAT 212  
 QY 61 PheProSerAspGlyHisCysValAspLeuProAspThrGlyLeuCysValGlySer 80  
 Db 213 TTCCCAAGTGCACAAAGGCGACTGCTGACCTGCGACACAGGACTTGCACAGAGC 272  
 QY 81 IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGly 100  
 Db 273 ATCCCGCTGTGTACTACACCCCTTCAGGACACTGCGCCGCTTACCTATGGTGT 332  
 QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120  
 Db 333 TGTATGGCAACAGAACAACTTTGAGGAGAGCAGCAGTGTCTGAGTCTTGTGCGGC 392  
 QY 121 IleSerLysLysAsnValPheGlyLeuArgGluIleProIleProSerThrGlySer 140  
 Db 393 ATCTCCAGAGAGATGTGTGGCTTGAGCGGGAATCCCATTCACGACAGGCTCT 452  
 QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160  
 Db 453 GTGGAGATGGCTGTGCGAGTGTCTCTGTCATCTGCTATGTGTGTGTAGCCATCTG 512  
 QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180  
 Db 513 GGTACTGCTCTTTCAGAGAACAGAGAAAGGACTTCCACGGA---CACAGCACACG 569  
 QY 181 ProThrProAlaSerSerThrValSerThrGluAspThrGluHisLeuValTyrAsn 200  
 Db 570 ACCAC---CTGCGCAGCTCCACTGTCTCCACTACCGAGGACACGAGCACTG-GTCTATAAC 627  
 QY 201 HisThrThrArgProLeu 206  
 Db 628 CACACACACGCGCCCTCTG 645

## RESULT 9

BG697670

LOCUS

DEFINITION

663 bp mRNA linear EST 07-MAY-2001

602660928P1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4803894 5',

mRNA sequence.

ACCESSION

BG697670

VERSION

BG697670.1 GI:13964146

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 663)

NIH-MGC <http://mgs.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: James Cleaver, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed By: The I.M.A.G.E. Consortium (LLNL) DNA  
 Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM10700 row: h column: 07  
 High quality sequence stop: 662.  
 Location/Qualifiers

1..663

## FEATURES

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4803894"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NCI CGAP Skn3"  
 /note="Organ: skin; Vector: pCMV-Sport6; Site 1: NCI;  
 Site 2: Salt; Cloned unidirectionally; primer: Oligo dT.  
 Average insert size 1.5kb Library constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

## Alignment Scores:

Pred. No.: 1,08e-95 Length: 663  
 Score: 1031.00 Matches: 185  
 Percent Similarity: 97.37% Conservatives: 0  
 Best Local Similarity: 97.37% Mismatches: 4  
 Query Match: 88.35% Indels: 1  
 DB: 12 Gaps: 0

US-09-935-390A-23 (1-206) x BG697670 (1-663)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
 Db 96 ATGGAAGGCGCCATCCAGTGTCTGCGACCTGTGAGCCACCACGATTCGCTGCAGC 155  
 QY 21 AsnGlyCysCysLeuAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40  
 Db 156 AATGGCTGTGTCATCGACAGTTCCTGAGTGTGACGACACCCCACTGCCCCGAGCC 215  
 QY 41 SerAspGluAlaAlaCysGluValThrSerGlyPheAspGluLeuGlnArgHis 60  
 Db 216 TCGACGAGCTGCTGTGAAATACAGAGTGTGTGACGAGCTCCAGCATTCAT 275  
 QY 61 PheProSerAspGlyHisCysValAspLeuProAspThrGlyLeuCysLysGlySer 80  
 Db 276 TTCCCAAGTGCACAAAGGCGACTGCTGACCTGCGACACAGGACTTGCACAGAGC 335  
 QY 81 IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGly 100  
 Db 336 ATCCCGCTGTGTACTACAAACCCCTTCAGCGAACACTGCGCCGCTTTACCTATGGTGT 395  
 QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120  
 Db 396 TGTATGGCAACAGAACAACTTTGAGGAGAGCAGAGTGTCTGAGTCTTGTGCGGC 455  
 QY 121 IleSerLysLysAspValPheGlyLeuArgGluIleProIleProSerThrGlySer 140  
 Db 456 ATCTCCAGAGAGATGTGTGGCTTGAGCGGGAATCCCATTCACGACAGGCTCT 515  
 QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160  
 Db 516 GTGGAGATGGCTGTGCGAGTGTCTGTGTCATCTGCAATTTGGTGTGGTAGCATCTTG 575  
 QY 161 GlyTyrCysPhePheLysAsnGlnArgLys-AspPheHisGlyHisHisHisProPr 180  
 Db 576 GGTACTGCTCTTTCAGAGAACAGAGAAACGAGCTTCCACGAGCACCATCATCAACAGC 635  
 QY 180 oProThrProAlaSerSerThrValSer 189  
 Db 636 AACCAACCCCTGCCAGCTCCACTGTCTCC



```

RESULT 10
BX336602
LOCUS
DEFINITION
BX336602 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
Clone CSODI030YE23 5-PRIME, mRNA sequence.
ACCESSION
BX336602
VERSION
BX336602.1 GI:30339518
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seq@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI030AC120P1&cluster=7854.f. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CSODI030AC12Q1.
Location/Qualifiers
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI030YE23"
/tissue_type="PLACENTA"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched. Double-strand cDNA was
digested with NotI and cloned into the NotI and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
FEATURES
source
ORIGIN
Alignment Scores:
Pred. No.: 8,67e-94 Length: 1201
Score: 1016.00 Matches: 181
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.45% Mismatches: 0
Query Match: 87.06% Indels: 0
DB: 13 Gaps: 0
US-09-935-390A-23 (1-206) x BX336602 (1-1201)
QY 25 IleAspSerPheLeuGluCysAspThrProAsnGlyPheAspAlaSerAspGluAla 44
DB 65 ATCGACAGTTTCCTGGAGTGTGACGACACCCCACTGCCCGGAGCGCTCCGAGGCT 124
QY 45 AlaCysGluIysTyrThrSerGlyPheAspGluLeuGlnArgIleHisPheProSerAsp 64
DB 125 GCCTGTGAATAATACACAGAGTGCTTTGACGAGCTCCAGGCTCCATTTCCCGAGCGAC 184
QY 65 LysGlyHisCysValAspLeuProAspThrGlyLeuCysGlyLeuSerIleProArgTyr 84
DB 185 AAAGGCGACTGCTGGACCTGCCACACAGAGGACTCTGCAGAGAGGACATCCCGCGCTGG 244
QY 85 TyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGlyCysTyrGlyAsn 104
DB 245 TACTACAACCCCTTCAGGACACTGCCCGCGCTTTTACCTATGCTGTTGTTATGCGAAC 304
QY 105 LysAsnAnPheGluGluGluGlnGlnCysLeuGluSerCysArgGlyIleSerIysIys 124
DB 305 AAGAACAACTTTGAGGAGAGCAGCAGTGTCTGAGTCTGTGCGGCGATCTCCAGAGAG 364
QY 125 AspValPheGlyLeuA-ArgGluIleProIleProSerThrGlySerValGluMetala 144

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DB 365 GATGTGTTGGCTGAGCGGGAATCCCATTCACACAGGCTCTGTGGAGTGGCT 424
QY 145 ValalaValPheLeuValIleCysIleValValValalalleLeuGlyTyrCysPhe 164
DB 425 GTCCAGTGTTCCTGGTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 494
QY 165 PheIysAsnGlnArgIysAspPheHisGlyHisHisHisHisHisHisHisHis 184
DB 485 TTTGAGAACCCAGAGAGGACTTCCAGGACACACACACACACACACACACAC 544
QY 185 SerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsnHisThrThrArg 204
DB 545 AGCTCCCACTGTCTCCACTACCGAGGACACGAGGACCTGGTCTATACACACAC 604
QY 205 ProLeu 206
DB 505 CCCCCTC 610
RESULT 11
BX336602
LOCUS
DEFINITION
BX336602 Homo sapiens cDNA clone IMAGE:3943699 5',
mRNA sequence.
ACCESSION
BX336602
VERSION
BX336602.1 GI:10216123
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 882)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LUCM99 row: f column: 20
High quality sequence stop: 766.
Location/Qualifiers
1..882
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3943699"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_hosts="DH10B (phage-resistant)"
/clone_lib="NIH-MGC_7"
/notes="Organ: lung; Vector: pOTS7; Site: 1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adapter: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using 2AP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

## ORIGIN

```

Alignment Scores:
Pred. No.: 3.33e-93 Length: 882
Score: 1008.50 Matches: 184
Percent Similarity: 92.20% Conservative: 5
Best Local Similarity: 89.76% Mismatches: 11
Query Match: 86.42% Indels: 5
DB: 10 Gaps: 2

```



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82..1605
/note="unnamed protein product; putative
serine protease inhibitor, Kunitz type 1
(MGP|MGI:1338033)"
/codon_start=1
/protein_id="BAB30697.1"
/db_xref="GI:12856531"
/translation="MAGRLARASISAVGWLLCALGLQNTAEKLPSPAEPLFGGRAC
LSRFTSGVFLDTEASVNGATFLGSPTRAGMDCVRSCTTQNCALVELQPDG
GDAISACFLANFYQNFVCKFAPKEGFINYLQELRYSELRITRFGSGRIPRIM
MGIDLKVLQKPLVADNADMLHLLQSDSDVRVERKRPEVELMGLKEGTLYFLQITR
TDSQPERETALITVLTAKTQEDYCLASYKVGRCGSPFRWYDPKEQICKX3FTFG
CLGNKNYLRBEZCKACKOVGSPKHHHPVCSCGCHATQFCNSCCIDGFLCDD
TPCPSDSDENICSKTSGFDELONIHFLSDKGYCALPDGFCCKENIPRWYXNPSE
CARPTGTCGCGNKKDFEEOCCLESCKSKDVPFGRREGSIPITVGSSEVALANVL
VICIIVLTILGICFFNQRKETHPLHPPPTPASSTVSTTEDEHLVNHNTQPL"
polyA_signal 2140..2145
/note="putative"
polyA_site 2155
/note="putative"

ORIGIN
Alignment Scores:
Pred. No.: 1.1e-91 Length: 2155
Score: 999.00 Matches: 173
Percent Similarity: 90.73% Conservative: 13
Best Local Similarity: 84.39% Mismatches: 19
Query Match: 85.60% Indels: 0
DB: 11 Gaps: 0

US-09-935-390A-23 (1-206) x AK017342 (1-2155)
QY 2 GluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSerAsn 21
DB 988 AAAAGGCCACCATCCAGTGTCTCCGGCAGCTGCCAGCCAGTTCGGCTGTAGCAAT 1047
QY 22 GlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAlaSer 41
DB 1048 GCGTCTGTATCGATGGCTTCTGGAGTGTGATGACAGCCAGAGTGCCTGATGGCTCC 1107
QY 42 AspGluAlaAlaCysGluIleYsThrSerGlyPheAspGluLeuGlnArgIleHisPhe 61
DB 1108 GACGAGGCCACCTGTGAAATATACACAGCGCTTTGATGAGCTTCAGAAATATCCATTTC 1167
QY 62 ProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSerIle 81
DB 1168 CTCAGTGACAAAGGTACTGTCCAGAGCTGCCAGACACTGGGTTTTCAGAGGAGAACATC 1227
QY 82 ProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyCys 101
DB 1228 CCACGCTGTATATACACCATTCAGTGAACCTGTGCCCGATTCCACCTATGGTGTTC 1287
QY 102 TyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGlyIle 121
DB 1288 TATGGGAACAGAACCACTTTGAGGAGGAGACAGCAGTGTCTTGTAGTCTGCCGTGGCATC 1347
QY 122 SerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySerVal 141
DB 1348 TCCAAAGAGGATGTGTTGTCTCTCGAGGGAAGGCTCCATTCCCACTGTAGGCTCCGCT 1407
QY 142 GluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeuGly 161
DB 1408 GAGGTAGCTATTGCTGTATTTCTGGTCATCTGCATCATAGTGTCTTAACCATCTCGGC 1467
QY 162 TyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisHisProPro 181
DB 1468 TACTGTTTCTTCAAGAACCAAGAAAGAAATTCACAGTCCCTCCAGCCACCCCTCC 1527
QY 182 ThrProAlaSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsnHis 201
DB 1528 ACACCGAGCCAGCTCCACTGTGTTCCACAGAGAGACAGAGACACTGCTCTATATAC 1587

```

```

QY 202 ThrThrArgProLeu 206
DB 1588 ACAACCCAGCTCTC 1602

RESULT 13
BX369479
LOCUS
DEFINITION
BX369479 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
Homo sapiens cDNA clone CS0DJ014YC20 5-PRIME, mRNA sequence.
ACCESSION
BX369479.1 GI:30457815
VERSION
BX369479.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 948)
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAF0362G12_AFO3456_1ccluster=7854.f.
Contact : Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAF0362G12_AFO3456_1.
Location/Qualifiers
1..948
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ014YC20"
/call_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
/note="First strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 2.34e-91 Length: 948
Score: 991.00 Matches: 190
Percent Similarity: 91.47% Conservative: 3
Best Local Similarity: 90.05% Mismatches: 12
Query Match: 84.92% Indels: 6
DB: 13 Gaps: 0

US-09-935-390A-23 (1-206) x BX369479 (1-948)
QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
DB 294 ATGGAAGGCCCATCCAGTGTGCTGTGGACCTGTGAGCCACCCAGTTCGGCTGAGC 353
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
DB 354 AATGGCTGTGCTGACGACAGTTCCTGGAGTGTGACGACACCCCACTGCCCGAGGCC 413
QY 41 SerAspGluAlaAlaCysGluIleYsThrSerGlyPheAspGluLeuGlnArgIleHis 60
DB 414 TCCGACGAGGCTGCTGTGAAATATACGAGTGGCTTTGACGAGCTCCAGCGCATCAT 473
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
DB 474 TTCCCCAGTGAAGAAGGCACTGTGGACCTGTGCAGACACAGGACTCTGCAAGAGAGC 533

```

/note="Organ: Prostate; Vector: pT73 Pac; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pT73 Pac vector. The library tag sequence located between the Not I site and the polyA tail is CCCAC. Tissue was provided by Tim Ratliff."

## ORIGIN

Alignment Scores: 7,46e-87 Length: 647  
 Pred. No.: 945.00 Matches: 173  
 Score: 945.00  
 Percent Similarity: 99.43% Conservative: 0  
 Best Local Similarity: 99.43% Mismatches: 1  
 Query Match: 80.98% Indels: 1  
 DB: 14 Gaps: 0

US-09-935-390A-23 (1-206) x CF146773 (1-647)

QY 33 AspThrProAsnGlySerProAspAlaSerGluAlaAlaCysGluLysThrSerGly 52  
 Db 8 GACACCCCAACTGCCCCGAGCGCTCCGAGGCTGCTGTGAATAA-ACAGTGGC 66  
 QY 53 PheAspGluLeuGlnArgIleHisPheProSerAspLysGlyHisCysValAspLeuPro 72  
 Db 67 TTGACGAGCTCCAGCGCATCCATTTCCCGAGTGCACAAAGGCGCTGGTGGACCTGCCA 126  
 QY 73 AspThrGlyLeuGlySerGlySerIleProArgTyrTyrTrpAsnProPheSerGluHis 92  
 Db 127 GACACGAGCTCTGCAAGGAGAGCATCCGCGCTGTACTACCAACCCCTTCAGCGAACAC 186  
 QY 93 CysAlaArgPheThrTyrGlyGlyCysTyrGlyValAsnLysAsnAsnPheGluGluGln 112  
 Db 187 TGGCCCGCTTACCTATGCTGTGTTATGGACACAGACCACTTTGAGGAGAGCAG 246  
 QY 113 GlnCysLeuGlySerCysArgGlyIleSerLysLysAspValPheGlyLeuArgGlu 132  
 Db 247 CAGTGCCTCGAGTCTTGTGCGGCATCTCCAGAGAGATGTGTGTTCCTGGCGCGGAA 306  
 QY 133 IleProIleProSerThrGlySerValGluMetAlaValAlaValPheLeuValIleCys 152  
 Db 307 ATCCCATTTCCAGCAGCAGCTCTGTGGAGATGGCTGCCAGTGTCTCTGTCATCTGC 366  
 QY 153 IleValValValAlaIleLeuGlyTyrCysPhePheLysAsnGlnArgLysAspPhe 172  
 Db 367 ATTGTGTGTGTAGCATCTTTGGTACTTCTTCAAGAACACAGAGAAAGGACTTC 426  
 QY 173 HisGlyHisHisHisProProThrProAlaSerSerThrValSerThrThrGlu 192  
 Db 427 CACGGACACCCACCCACCCACCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAG 486  
 QY 193 AspThrGluHisLeuValTyrAsnHisThrThrArgProLeu 206  
 Db 487 GACACGAGGACCTGTGCTATATACACACACCCCGGCCCTC 528

RESULT 15  
 BX334952/c

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1201 bp mRNA linear EST 01-MAY-2003  
 BX334952 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
 clone CS0DI009YC11 3-PRIME, mRNA sequence.

EX334952 GI:30310380

EST.

Homo sapiens (human)

Homo sapiens

Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100  
 Db 534 ATCCCGGCTGTACTACAAACCCCTTCAGCGAACACATCGCCCGCTTTAACCATTGTGGT 593  
 QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysValLeuGluSerCysArgGly 120  
 Db 594 TGTATGGCAACAGAACAACTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 653  
 QY 121 IleSerLysLysAspValPheGlyLeuArgGluIleProIleProSerThrGlySer 140  
 Db 654 ATCTNCAAGAGGATGTGTGGCTCGAGCGGGAATCCCATTCGCCAGACAGGCTCT 713  
 QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLe 160  
 Db 714 GTGAGATGGCTGCGAGATGTTCTGTGTCATCTGCAATGGGTGTGTAGCCATCTT 773  
 QY 160 uGlyTyrCysPhePheLysAsnGlnArgLysAspPheHis-GlyHisHisHisHisProp 180  
 Db 774 TGGTTACTGGTCTTTCAAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 833  
 QY 180 roProThrProAlaSerSerThrValSerThrThrGluAsp-ThrGluHis-LeuVal 199  
 Db 834 CAACCAACCTTGGCAGTTCCTTCTTACTACCCGAGGACACCGGACCCCTGTCT 893  
 QY 199 YrAsnHisThr-ThrArgPro 205  
 Db 894 TTAACCAACCCACCCGCGCC 914

## RESULT 14

CF146773

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CF146773 647 bp mRNA linear EST 06-AUG-2003  
 UI-HF-CBO-atd-a-02-0-UI-ri NIH MGC\_210 Homo sapiens cDNA clone  
 IMAGE:30570529 5', mRNA sequence.

CF146773

CF146773.1 GI:33262217

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 647)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MBERF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Tim Ratliff

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/humanfl.html

The following repetitive elements were found in this cDNA

sequence: 426-483, >(TGG)#Simple\_repeat (matched complement)

Seq primer: PYX-5.

Location/Qualifiers

1..647

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:30570529"

/tissue\_type="CNCAP(3)T-225 cell line"

/lab\_host="DH10B (T1 phage resistant)"

/clone\_lib="NIH\_MGC\_210"

## FEATURES

source

## TITLE Full-length cDNA libraries and normalization

Unpublished (2001)

## COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7854.f For more information about this cluster, see

<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0D1009AB06NP1&cluster=7854.f>Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/>

Paraday Avenue Genoscope sequence ID : CS0D1009AB06NP1.

Location/Qualifiers

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## FEATURES

source

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0D1009YC11"

/tissue\_type="PLACENTA COT 25-NORMALIZED"

/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

## Alignment Scores:

Pred. No.:	4.5e-81	Length:	1201
Score:	892.50	Matches:	168
Percent Similarity:	92.35%	Conservative:	1
Best Local Similarity:	91.80%	Mismatches:	13
Query Match:	76.48%	Indels:	2
DB:	13	Gaps:	1

US-09-935-390A-23 (1-206) x BX334952 (1-1201)

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Qy	44	AlaAlaCysGluLysThrSerGlyPheAspGluLeuGlnArgIleHisPheProSer	63
Db	1133	GCTGCCTNTGAAAAATACGAGTGGCTTTGACGAGTCCAGCGCATCCATTTCCCGAGT	1074
Qy	64	AspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSerIleProArg	83
Db	1073	GACAAAGGGGCTGCGTGGACWTGCCAGACAGACTCTGCAGAGAGAGCTCCCGGC	1014
Qy	84	TrpTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyCysTyrGly	103
Db	1013	TGGTACTACACCCCTTCAGCGACACTGCGCCGCTTTACCTATGGTGGTTGTTATGCG	954
Qy	104	AsnLysAsnAsnPheGluGluGlnCysLeuGluSerCysArgGlyIleSerLys	123
Db	953	AACAAGACAACTTGGAGAGAGAGAGAGAGTCTCGAGTCTTGTGCGGCACTCCCAAG	894
Qy	124	LysAspValPheGlyLeuArgGluIleProIleProSerThrGlySerValGluMet	143
Db	893	AAGGATGTCTTGGCTCTGAGCGGGAATCCCATTCACACAGGCTCTGTGGAGATG	834
Qy	144	AlaValAlaValPheLeuValIleCysIleValValValAlaIleLeuGlyTyrCys	163
Db	833	ST-GTCCGAGTGTCTCTGTCATCTGCAATTGGTGGTGGTAGCCATCTTGGGTACTGC	775
Qy	164	PhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProProThrPro	183
Db	774	TTCCTTCAAGACCAAGAGACTTCCAGGACACACACACACACACACACACCCCT	715
Qy	184	AlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsnHisThrThr	203
Db	714	GCCAGCTCCACTGTCTCCACTACCGAGGACACGAGCMCTGCTATATACACACACC	655

Qy 204 ArgProLeu 206

Db 654 CGGCCCTC 646

Search completed: April 22, 2004, 10:13:59

Job time : 2508 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 22, 2004, 08:23:19 ; Search time 413 Seconds  
(without alignments)  
2248.855 Million cell updates/sec

Title: US-09-935-390A-23  
Perfect score: 1167  
Sequence: 1 MERRHVCSTGCTQTCRCS.....TVSTTDETHLVNHTREL 206

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/cgn2\_1/USPTO.spool/US09935390 -QFMT=fastap -SUFFIX=usnnpb -MINMATCH=0.1  
-DB=Published Applications NA -QFMT=fastap -SUFFIX=usnnpb -MINMATCH=0.1  
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62  
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Database : Published Applications NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	ID	Description
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1	1167	100.0	1505	9	US-09-935-390A-4	Sequence 4, Appli
2	1167	100.0	1542	9	US-09-765-449-8	Sequence 8, Appli
3	1163	99.7	2482	9	US-09-742-201-1	Sequence 1, Appli
4	1163	99.7	2482	13	US-10-081-056-41	Sequence 41, Appl
5	1163	99.7	2482	13	US-10-245-752-9	Sequence 9, Appli
6	1163	99.7	2482	13	US-10-245-859-9	Sequence 9, Appli
7	1163	99.7	2482	13	US-10-211-858-11	Sequence 11, Appl
8	1163	99.7	2482	13	US-10-305-654-41	Sequence 41, Appl
9	1163	99.7	2482	15	US-10-245-103-9	Sequence 9, Appli
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41	1163	99.7	2482	15	US-10-237-636-9	Sequence 9, Appli
42	1163	99.7	2482	15	US-10-238-325-9	Sequence 9, Appli
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ALIGNMENTS

RESULT 1  
US-09-935-390A-4  
Sequence 4, Application US/09935390A  
Patent No. US20020076761A1  
GENERAL INFORMATION:  
APPLICANT: Escobedo, Jaime  
Quianjin, Hu  
Garcia, Pablo  
Williams, Lewis T.  
Kochakota, Srinivas  
TITLE OF INVENTION: Secreted Human Proteins  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/935,390A
FILING DATE: 22-AUG-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/988,671
FILING DATE: 1997-12-11
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. R. Potter
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 1369.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2718
TELEFAX: (510) 655-3542
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1505 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-935-390A-4

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Alignment Scores:
Pred. No.: 4.36e-145 Length: 1505
Score: 1167.00 Matches: 206
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DB: Gaps: 0

US-09-935-390A-23 (1-206) x US-09-935-390A-4 (1-1505)

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Qy 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
Db 231 AATGGCTGCTGCAATGCACAGTTCTCGAGTGTGCACACCCCCCACTGCCCGACGCC 290
Qy 41 SerAspGluAlaAlaCysGluysTyThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 291 TCCAGAGCGCTGCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCAATCCAT 350
Qy 61 PheProSerAspIysGlyHisCysValAspLeuProAspThrGlyLeuCysIysGluSer 80
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Qy 81 IleProArgTrpTyTrpAsnProPheSerGluHisCysAlaArgPheThrTyThrGlyGly 100
Db 411 ATCCCGCGTGGTACTACAAACCCCTTCAGCGAACACACTGCGCGCGCTTTTACCTATGTGGT 470
Qy 101 CysTyrglyAsnIysAsnAsnPheGluGluGlnGlnCysValLeuGluSerCysArgGly 120
Db 471 TGTATCGGCACACAGAAACACTTTGAGGAGAGGACAGTGCCTCGAGTCTGTTCGGCGGC 530
Qy 121 IleSerIysIysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
Db 531 ATCTCCAAGAAGATGTGTTGGCTGAGGGGGGAAATCCCATTTCCAGCACAGGCTCT 590
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1 DB      711 CCCACCCCTGCAGCTCCACTGTCTCCACTACCGAGGACACGAGCCTGCTCTATAAC 770
2
3 QY      201 HisThrThrArgProLeu 206
4          |||||
5 DB      771 CACACACAGCGGCCCCCTC 788
6
7 RESULT 2
8 US-09-765-449-8
9 ; Sequence 8, Application US/09765449
10 ; Patent No. US20020098537A1
11 ; GENERAL INFORMATION:
12 ; APPLICANT: SHIMOMURA, Takeshi
13 ;             KAWAGUCHI, Toshiya
14 ;             KITAMURA, Naomi
15 ;             MIYAZAWA, Keiji
16 ; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
17 ;                     AND METHOD OF PRODUCING THE PROTEIN
18 ;
19 ; NUMBER OF SEQUENCES: 18
20 ; CORRESPONDENCE ADDRESS:
21 ; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
22 ; STREET: 2100 Pennsylvania Avenue, N.W.
23 ; CITY: Washington
24 ; STATE: DC
25 ; COUNTRY: USA
26 ; ZIP: 20037
27 ; COMPUTER READABLE FORM:
28 ; MEDIUM TYPE: Floppy Disk
29 ; COMPUTER: IBM PC compatible
30 ; OPERATING SYSTEM: PC-DOS/MS-DOS
31 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
32 ; CURRENT APPLICATION DATA:
33 ; APPLICATION NUMBER: US/09765,449
34 ; FILING DATE: 22-Jan-2001
35 ; PRIOR APPLICATION DATA:
36 ; APPLICATION NUMBER: 08/685,558
37 ; FILING DATE: <Unknown>
38 ; INFORMATION FOR SEQ ID NO: 8
39 ; SEQUENCE CHARACTERISTICS:
40 ;     LENGTH: 1542 base pairs
41 ;     TYPE: nucleic acid
42 ;     STRANDEDNESS: double
43 ;     TOPOLOGY: linear
44 ;     MOLECULE TYPE: CDNA to mRNA
45 ;     ANTI-SENSE: no
46 ;     ORIGINAL SOURCE:
47 ;         ORGANISM: Homo sapiens
48 ;         STRAIN: MKN45
49 ;         FEATURES:
50 ;             (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 8
51 ;
52 US-09-765-449-8

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Alignment Scores:			
Pred. No.:	4.52e-145	Length:	1542
Score:	1167.00	Matches:	206
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0
US-09-935-390A-23 (1-206) x US-09-765-449-8 (1-1542)			
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Qy	21	AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla	40
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Qy	41	SerAspGluAlaIaCysGluLyTyThrSerGlyPheAspGlnLeuGlnArgIleHis	60
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1 PRIOR APPLICATION NUMBER: PCT/US00/20710  
2 PRIOR FILING DATE: 2000-07-28  
3 PRIOR APPLICATION NUMBER: US 60/222,695  
4 PRIOR FILING DATE: 2000-08-02  
5 PRIOR APPLICATION NUMBER: US 09/643,657  
6 PRIOR FILING DATE: 2000-08-17  
7 PRIOR APPLICATION NUMBER: PCT/US00/23522  
8 PRIOR FILING DATE: 2000-08-23  
9 PRIOR APPLICATION NUMBER: PCT/US00/23328  
10 PRIOR FILING DATE: 2000-08-24  
11 PRIOR APPLICATION NUMBER: US 60/230,978  
12 PRIOR FILING DATE: 2000-09-07  
13 PRIOR APPLICATION NUMBER: US 60/000,000  
14 PRIOR FILING DATE: 2000-09-15  
15 PRIOR APPLICATION NUMBER: US 09/664,610  
16 PRIOR FILING DATE: 2000-09-18  
17 PRIOR APPLICATION NUMBER: US 09/665,350  
18 PRIOR FILING DATE: 2000-09-18  
19 PRIOR APPLICATION NUMBER: US 60/242,922  
20 PRIOR FILING DATE: 2000-10-24  
21 PRIOR APPLICATION NUMBER: US 09/709,238  
22 PRIOR FILING DATE: 2000-11-08  
23 PRIOR APPLICATION NUMBER: PCT/US00/30952  
24 PRIOR FILING DATE: 2000-11-08  
25 PRIOR APPLICATION NUMBER: PCT/US00/30873  
26 PRIOR FILING DATE: 2000-11-10  
27 PRIOR APPLICATION NUMBER: PCT/US00/32678  
28 PRIOR FILING DATE: 2000-12-01  
29 PRIOR APPLICATION NUMBER: US 09/747,259  
30 PRIOR FILING DATE: 2000-12-20  
31 PRIOR APPLICATION NUMBER: PCT/US00/34956  
32 PRIOR FILING DATE: 2000-12-20  
33 PRIOR APPLICATION NUMBER: US 09/767,609  
34 PRIOR FILING DATE: 2001-01-22  
35 PRIOR APPLICATION NUMBER: US 09/796,498  
36 PRIOR FILING DATE: 2001-02-28  
37 PRIOR APPLICATION NUMBER: PCT/US01/06520  
38 PRIOR FILING DATE: 2001-02-28  
39 PRIOR APPLICATION NUMBER: PCT/US01/06666  
40 PRIOR FILING DATE: 2001-03-01  
41 PRIOR APPLICATION NUMBER: US 09/802,706  
42 PRIOR FILING DATE: 2001-03-09  
43 PRIOR APPLICATION NUMBER: US 09/808,689  
44 PRIOR FILING DATE: 2001-03-14  
45 PRIOR APPLICATION NUMBER: US 09/816,744  
46 PRIOR FILING DATE: 2001-03-22  
47 PRIOR APPLICATION NUMBER: US 09/828,366  
48 PRIOR FILING DATE: 2001-04-05  
49 PRIOR APPLICATION NUMBER: US 09/854,208  
50 PRIOR FILING DATE: 2001-05-10  
51 PRIOR APPLICATION NUMBER: US 09/854,280  
52 PRIOR FILING DATE: 2001-05-10  
53 PRIOR APPLICATION NUMBER: US 09/866,028  
54 PRIOR FILING DATE: 2001-05-25  
55 PRIOR APPLICATION NUMBER: US 09/866,034  
56 PRIOR FILING DATE: 2001-05-25  
57 PRIOR APPLICATION NUMBER: PCT/US01/17092  
58 PRIOR FILING DATE: 2001-05-25  
59 PRIOR APPLICATION NUMBER: US 09/870,574  
60 PRIOR FILING DATE: 2001-05-30  
61 PRIOR APPLICATION NUMBER: PCT/US01/17443  
62 PRIOR FILING DATE: 2001-05-30  
63 PRIOR APPLICATION NUMBER: PCT/US01/17800  
64 PRIOR FILING DATE: 2001-06-01  
65 PRIOR APPLICATION NUMBER: PCT/US01/19692  
66 PRIOR FILING DATE: 2001-06-20  
67 PRIOR APPLICATION NUMBER: PCT/US01/00000  
68 PRIOR FILING DATE: 2001-06-28  
69 NUMBER OF SEQ ID NOS: 383  
70  
71 SEQ ID NO 41  
72  
73 LENGTH: 2482  
74 TYPE: DNA  
75 ORGANISM: Homosapiens

US-10-081-056-41

Alignment Scores: 3.12e-144 Length: 2482  
Pred. No.: 1163.00 Matches: 205  
Score: 99.51% Conservatives: 1  
Percent Similarity: 99.51% Mismatches: 0  
Best Local Similarity: 99.66% Indels: 0  
Query Match: 13 Gaps: 0  
DB: 13

US-09-935-390A-23 (1-206) x US-10-081-056-41 (1-2482)

Qy 1 MetGluArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
Db 1157 ATGAAAAGCGCCATCCAGTGTCTCTGTCACCTGTGAGCCACCCAGTTCCTGTCAGC 1216  
Qy 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40  
Db 1217 ATGGCTGCTGCAATCGACAGTTTCTTGGAGTGTGACGACACCCCACTGCCCCGAGCC 1276  
Qy 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60  
Db 1277 TCCGACGAGGCTGCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCAT 1336  
Qy 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
Db 1337 TTCCCCAGTGACAAAGGCGCACTGCGTGAGCTTCCAGACAGAGACTCTCCAGGAGAGC 1396  
Qy 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100  
Db 1397 ATCCCGCGCTGCTACTACAAACCCCTTCAGCGAACACATGCGCGCGCTTACCTATGTTGT 1456  
Qy 101 CysTyrGlyAsnLysAsnAsnAspGluGluGlnGlnCysLeuGluSerCysArgGly 120  
Db 1457 TGTATGGCAACAGAACTTTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1516  
Qy 121 IleSerLysLysAspValPheGlyLeuArgGluLeuProIleProSerThrGlySer 140  
Db 1517 ATCTCCAGAGAGAGTGTGTTGGCTGAGGCGGGAATCCCATTCACGACAGCAGGCTCT 1576  
Qy 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160  
Db 1577 GTGGAGATGGCTGTACAGAGTGTCTGCACTATCTGCAATGTGGTGGTGGTGGTGGTGG 1636  
Qy 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180  
Db 1637 GGTACTGCTCTTTCAGAACACAGAGAGAGACTTCCACGAGACACACACACACACCA 1696  
Qy 181 ProThrProAlaSerSerThrValSerThrGluAspThrGluHisLeuValTyrAsn 200  
Db 1697 CCCACCCCTGCCAGTCCACTGTCTCCACTACCGAGGACACGAGGACCTGGTCTATAAC 1756  
Qy 201 HistThrArgProLeu 206  
Db 1757 CACACACCCCGGCCCTC 1774

RESULT 5

US-10-245-752-9  
Sequence 9, Application US/10245752  
Publication No. US20030064473A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Baton, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630RIC66
; CURRENT APPLICATION NUMBER: US/10/245,752
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 9
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-752-9

Alignment Scores:
Pred. No.: 3,12e-144 Length: 2482
Score: 1163.00 Matches: 205
Percent Similarity: 99.51% Conservatives: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
DB: 13 Gaps: 0

US-09-935-390A-23 (1-206) x US-10-245-752-9 (1-2482)

Qy 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 1157 ATGGAAGGCCCATCCAGTGTCTGTGGACCTGTTCAGCCACCCAGTTCCTGCGTGCAGC 1216

Qy 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
Db 1217 AATGCTCTGATCCAGAGTTCTTGAGTGTGACGACACCCCACTGCCCCGACGCC 1276

Qy 41 SerAspGluAlaAlaCysGluLysTyThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 1277 TCCGACGAGGCTGCTGTGAAAAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1336

Qy 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 1337 TTCGCCAGGACAAAGGGGACTGCTGGACCTGCCAGACACAGGACTCTGCAAGGAGGC 1396

Qy 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 1397 ATCCCGCGCTGTACTACAAACCTTCAGCGAACACTCCGCGCTTTACCTATGTGTGT 1456

Qy 101 CysTyrGlyAsnLysAsnAsnPheGluGlnGlnCysLeuGluSerCysArgGly 120
Db 1457 TGTATGGCAACAAGAACACTTTGAGGAGGACGAGTGCCTCGAGTCTTGCGCGGC 1516

Qy 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
Db 1517 ACTTCAGAGAGTGTGTTGGCTTGGCGGGAAATCCCATTTCCAGCAGCAGGCTCT 1576

Qy 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160

Db 1577 GTGGAGATGGCTGTCCACAGTGTTCCTGTCTCATCTGCATTTGGTGGTGGTAGCCATCTTG 1636
Qy 161 GlyTyrCysPhePheLeuAsnGluArgLysAspPheHisGlyHisHisHisProPro 180
Db 1637 GGTACTGCTTCTTCAGAACCCAGAGAAAGGACTTCCAGGACACCAACCCACCA 1696
Qy 181 ProThrProAlaSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
Db 1697 CCAACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGAGACCTGTGTCTATAAC 1756
Qy 201 HisThrThrArgProLeu 206
Db 1757 CACACACCCCGCCCTC 1774

RESULT 6
US-10-245-859-9
; Sequence 9: Application US/10245859
; Publication No. US2003006447A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630RIC78
; CURRENT APPLICATION NUMBER: US/10/245,859
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 9
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-859-9

Alignment Scores:
Pred. No.: 3,12e-144 Length: 2482
Score: 1163.00 Matches: 205
Percent Similarity: 99.51% Conservatives: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
DB: 13 Gaps: 0

US-09-935-390A-23 (1-206) x US-10-245-859-9 (1-2482)

QY 1 MetGluArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
 Db 1157 ATGAAAGGCGCCATCCAGTGTCTCTGCACTGACCCAGCCAGTTCGGCTGCAGC 1216  
 QY 21 AsnGlyCysCysLeuAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40  
 Db 1217 AATGGCTGCTGCTACAGAGTTTCTCGAGTGTGACGACACCCCAACTGCCCGGACGCC 1276  
 QY 41 SerAspGluAlaAlaCysGluTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60  
 Db 1277 TCCGAGGAGGCTGCTGTGAAATAACAGAGTGGCTTTGACGAGCTCCAGCGCATCAT 1336  
 QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysIleGluSer 80  
 Db 1337 TTCCCAAGTACAAAGGCGACCTCGGAGACCTGCCAGACAGGACTCTGCAAGGAGGC 1396  
 QY 81 IleProArgTyrThrValSerPheSerGluHisCysAlaArgPheThrTyrGlyGly 100  
 Db 1397 ATCCCGCGCTGGTACTACAAACCTTCAGCGAACACTGCGCGGCTTTTACCTATGTTG 1456  
 QY 101 CysTyrGlyAsnLysAsnAspPheGluGluGlnGlnCysLeuGluSerCysArgGly 120  
 Db 1457 TGTATGGCAACAGAACACTTTGAGGAGAGGAGCAGTGGCTCGAGTCTTTGCGGGC 1516  
 QY 121 IleSerLysAspValPheGlyLeuArgGluIleProIleProSerThrGlySer 140  
 Db 1517 ATCTCAAGAGGATGTGTTGGCTGAGCGCGGAAATCCCATTTCCAGCACAGGCTCT 1576  
 QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160  
 Db 1577 GTGAGATGGCTGTACAGTGTCTCGTCACTGCTGATTTGGTGGTGGTATCTTG 1636  
 QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180  
 Db 1637 GGTACTGCTTCTTCAAGAACAGAGAGAGGAGCTTCCAGGACACCAACCAACCCACCA 1696  
 QY 181 ProThrProAlaSerSerThrValSerThrGluAspThrGluHisLeuValTyrAsn 200  
 Db 1697 CCACCCCTGCGAGCTTCCACTGCTCCACTACCGAGGACAGGAGCCTGGTCTATAAC 1756  
 QY 201 HisThrArgProLeu 206  
 Db 1757 CACACCAACCGGCGCCCTC 1774

## RESULT 7

US-10-211-858-11  
 ; Sequence 11, Application US/10211858  
 ; Publication No. US20030211096A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Warsters, Scott A.  
 ; APPLICANT: Fan, James  
 ; APPLICANT: Pitti, Robert M.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stone, Donna M.  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR  
 ; FILE REFERENCE: P293IRIC1  
 ; CURRENT APPLICATION NUMBER: US/10/211,858  
 ; CURRENT FILING DATE: 2003-08-02  
 ; PRIOR APPLICATION NUMBER: 60/014699  
 ; PRIOR FILING DATE: 1996-04-01  
 ; PRIOR APPLICATION NUMBER: 60/026943  
 ; PRIOR FILING DATE: 1996-09-23  
 ; PRIOR APPLICATION NUMBER: 60/059121  
 ; PRIOR FILING DATE: 1997-07-17

; PRIOR APPLICATION NUMBER: 60/059352  
 ; PRIOR FILING DATE: 1997-09-19  
 ; PRIOR APPLICATION NUMBER: 60/062037  
 ; PRIOR FILING DATE: 1997-10-10  
 ; PRIOR APPLICATION NUMBER: 60/063755  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/063045  
 ; PRIOR FILING DATE: 1997-10-24  
 ; PRIOR APPLICATION NUMBER: 60/063046  
 ; PRIOR FILING DATE: 1997-10-24  
 ; PRIOR APPLICATION NUMBER: 60/066511  
 ; PRIOR FILING DATE: 1997-11-24  
 ; PRIOR APPLICATION NUMBER: 60/066772  
 ; PRIOR FILING DATE: 1997-11-24  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 258  
 ; SEQ ID NO 11  
 ; LENGTH: 2482  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-211-858-11  
 Alignment Scores:  
 Pred. No.: 3,12e-144 Length: 2482  
 Score: 1163.00 Matches: 205  
 Percent Similarity: 99.51% Conservative: 0  
 Best Local Similarity: 99.51% Mismatches: 1  
 Query Match: 99.66% Indels: 0  
 DB: 13 Gaps: 0  
 US-09-935-390A-23 (1-206) x US-10-211-858-11 (1-2482)  
 QY 1 MetGluArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
 Db 1157 ATGAAAGGCGCCATCCAGTGTCTCTGCACTGACCCAGCCAGTTCGGCTGCAGC 1216  
 QY 21 AsnGlyCysCysLeuAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40  
 Db 1217 AATGGCTGCTGCTACAGAGTTTCTCGAGTGTGACGACACCCCAACTGCCCGGACGCC 1276  
 QY 41 SerAspGluAlaAlaCysGluTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60  
 Db 1277 TCCGAGGAGGCTGCTGTGAAATAACAGAGTGGCTTTGACGAGCTCCAGCGCATCAT 1336  
 QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysIleGluSer 80  
 Db 1337 TTCCCAAGTACAAAGGCGACCTCGGAGACCTGCCAGACAGGACTCTGCAAGGAGGC 1396  
 QY 81 IleProArgTyrThrValSerThrGluHisCysAlaArgPheThrTyrGlyGly 100  
 Db 1397 ATCCCGCGCTGGTACTACAAACCTTCAGCGAACACTGCGCGGCTTTTACCTATGTTG 1456  
 QY 101 CysTyrGlyAsnLysAsnAspPheGluGluGlnGlnCysLeuGluSerCysArgGly 120  
 Db 1457 TGTATGGCAACAGAACACTTTGAGGAGAGGAGCAGTGGCTCGAGTCTTTGCGGGC 1516  
 QY 121 IleSerLysAspValPheGlyLeuArgGluIleProIleProSerThrGlySer 140  
 Db 1517 ATCTCAAGAGGATGTGTTGGCTGAGCGCGGAAATCCCATTTCCAGCACAGGCTCT 1576  
 QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160  
 Db 1577 GTGAGATGGCTGTACAGTGTCTCGTCACTGCTGATTTGGTGGTGGTATCTTG 1636  
 QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180  
 Db 1637 GGTACTGCTTCTTCAAGAACAGAGAGGAGCTTCCAGGACACCAACCAACCCACCA 1696  
 QY 181 ProThrProAlaSerSerThrValSerThrGluAspThrGluHisLeuValTyrAsn 200  
 Db 1697 CCACCCCTGCGAGCTTCCACTGCTCCACTACCGAGGACAGGAGCCTGGTCTATAAC 1756  
 QY 201 HisThrArgProLeu 206

[illegible]

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DB:
US-09-935-390A-23 (1-206) x US-10-245-103-9 (1-2482)
QY 1 MetGluArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
DB 1157 ATGGAAGGCGCATCCAGTGTCTGTGCACCTGTGCAGCCACCCAGTTCGGTGCAGC 1216
QY 21 AsnGlyCysCysLeuAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
DB 1217 AATGGCTGTGCATCGACAGTTCTCTGGAGTGTGACGACACCCCACTGCGCCGAGCC 1276
QY 41 SerAspGluAlaAlaCysGluValThrSerGlyPheAspGluLeuGlnArgIleHis 60
DB 1277 TCCGACGAGCTGCTGTGAAATAACACAGTGTCTTGACGAGCTCCACGCGCATCAT 1336
QY 61 PheProSerAspGlyHisCysValAspLeuProAspThrGlyLeuCysGlySer 80
DB 1337 TTCCCACTGACAAAGCGCACTGCTGACCTGACGACACACAGGACTCTGCAAGGAGAGC 1396
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
DB 1397 ATCCCGCTGTGTACTACAACTTTCAGCGAACACTGCGCCGCTTTTACCTATGTGGT 1456
QY 101 CysTyrGlyAsnLysAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
DB 1457 TGTATGGCAACAAGAACTTTGAGGAAGACGACGAGTGCCTCGAGTCTTGTGCGGC 1516
QY 121 IleSerGlyAspValPheGlyLeuArgGluIlePheProSerThrGlySer 140
DB 1517 ATCTCCAGAGAGTGTGTGTGGCTGTGAGCGGGAAATCCCATTTCCAGCACAGGCTCT 1576
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
DB 1577 GTGGAGATGGCTGTACAGTGTCTCTGTGTCATCTGCTGTGTGGTGTGGTATCTTG 1636
QY 161 GlyTyrCysPhePheValAsnGlnArgLysAspPheHisGlyHisHisHisHisProPro 180
DB 1637 GGTACTGTCTTCTTCAAGAACACAGAGAAGAGACTTCCAGGACACACACACACACCA 1696
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
DB 1697 CCCACCTTCCAGCTCCACTGTCTCCACTACCGAGGACACGAGGACCTGTGTCTATAAC 1756
QY 201 HistThrArgProLeu 206
DB 1757 CACACACCGCGCCCTC 1774

RESULT 10
US-10-245-107-9
; Sequence 9, Application US/10245107
; Publication No. US20030068779A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P36301C71
; CURRENT APPLICATION NUMBER: US/10/245,107
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114

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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 9
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-107-9

```

```

Alignment Scores:
Pred. No.: 3,12e-144 Length: 2482
Score: 1163.00 Matchee: 205
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
DB: 15 Gaps: 0

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US-09-935-390A-23 (1-206) x US-10-245-107-9 (1-2482)

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QY 1 MetGluArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
DB 1157 ATGGAAGGCGCATCCAGTGTCTGTGCACCTGTGCAGCCACCCAGTTCGGTGCAGC 1216
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
DB 1217 AATGGCTGTGCATCGACAGTTCTCTGGAGTGTGACGACACCCCACTGCGCCGAGCC 1276
QY 41 SerAspGluAlaAlaCysGluValThrSerGlyPheAspGluLeuGlnArgIleHis 60
DB 1277 TCCGACGAGCTGCTGTGAAATAACACAGTGTCTTGACGAGCTCCACGCGCATCAT 1336
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysGlySer 80
DB 1337 TTCCCACTGACAAAGCGCACTGCTGACCTGACGACACACAGGACTCTGCAAGGAGAGC 1396
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
DB 1397 ATCCCGCTGTGTACTACAACTTTCAGCGAACACTGCGCCGCTTTTACCTATGTGGT 1456
QY 101 CysTyrGlyAsnLysAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
DB 1457 TGTATGGCAACAAGAACTTTGAGGAAGACGACGAGTGCCTCGAGTCTTGTGCGGC 1516
QY 121 IleSerGlyAspValPheGlyLeuArgGluIlePheProSerThrGlySer 140
DB 1517 ATCTCCAGAGAGTGTGTGTGGCTGTGAGCGGGAAATCCCATTTCCAGCACAGGCTCT 1576
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
DB 1577 GTGGAGATGGCTGTACAGTGTCTCTGTGTCATCTGCTGTGTGGTGTGGTATCTTG 1636
QY 161 GlyTyrCysPhePheValAsnGlnArgLysAspPheHisGlyHisHisHisHisProPro 180
DB 1637 GGTACTGTCTTCTTCAAGAACACAGAGAAGAGACTTCCAGGACACACACACACACCA 1696
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200

```

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Db 1697 CCCACCCCTGCGAGCTCCACTGTCTCCACTACCGAGGACACGAGCACTGTGTATTAAC 1756
Qy 201 HisThrThrArgProLeu 206
Db 1757 CACACACCCGCGCCCTC 1774

RESULT 11
US-10-245-143-9
; Sequence 9, Application US/10245143
; Publication No. US20030068780A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630RIC90
; CURRENT APPLICATION NUMBER: US/10/245,143
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 9
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-143-9

Alignment Scores:
Pred. No.: 3,12e-144 Length: 2482
Score: 1163.00 Matches: 205
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
DB: 15 Gaps: 0

US-09-935-390A-23 (1-206) x US-10-245-143-9 (1-2482)
Qy 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 1157 ATGGAAGGGGCCATCCAGTGTCTCTGGCACCTGTTCAGCCCACTCCGCTCGAGC 1216
Qy 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
Db 1217 AATGCTGCTGCATCGACAGTTCTCTGGAGTGTGACGACACCCCACTGCCCGAGGCC 1276
```

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Qy 41 SerAspGluAlaAlaCysGluLysTyThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 1277 TCCGACGAGGCTGCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1336
Qy 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 1337 TTCCCGAGTGCACAAAGGCACTGCTGGACCTGCGACACACAGGACTCTGCAAGGAGAGC 1396
Qy 81 IleProArgTrpTyThrAsnProPheSerGluHisCysAlaArgPheThrTyThrGlyGly 100
Db 1397 ATCCCGGCGCTGTAATAACACCCCTTCAGCGAACACTGCGCGCCGCTTTACCTATGTTGGT 1456
Qy 101 CysTyrglyAsnLysAsnAsnPhelGluGlnGlnCysLeuGluSerCysArgGly 120
Db 1457 TGTTATGGCAACAGAACAACTTTGAGGAGAGGACGAGCTGCTCGAGTCTTGTTCGCGGC 1516
Qy 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
Db 1517 ATCTCCAGAGAGTGTGTTTGGCTGTAGGGCGGGAATCCCAATTCAGCAGCAGCTCT 1576
Qy 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
Db 1577 GTGGAGATGGCTGTACACAGTGTCTCTGCTCATCTGATTTGGTGTGTGTAGCCATCTTG 1636
Qy 161 GlyTyrcysPhePheLysAsnGluArgLysAspPheHisGlyHisHisProPro 180
Db 1637 GGTACTCTCTCTTCACAGACACGAGAAAGGACTTCCACGAGACACACACACCCACCA 1696
Qy 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisValTyran 200
Db 1697 CCCACCCCTGCGAGCTCCACTGTCTCCACTACCGAGGACACGAGCAGCTGTGTATTAAC 1756
Qy 201 HisThrThrArgProLeu 206
Db 1757 CACACACCCGCGCCCTC 1774

RESULT 12
US-10-245-771-9
; Sequence 9, Application US/10245771
; Publication No. US20030068781A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630RIC98
; CURRENT APPLICATION NUMBER: US/10/245,771
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 9
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-143-9
```

APPLICANT: Baker, Kevin  
APPLICANT: Baton, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Phillippe  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C93  
CURRENT APPLICATION NUMBER: US/10/245,851  
CURRENT FILING DATE: 2002-09-16  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/055027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 9  
LENGTH: 2482  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-245-771-9

Alignment Scores:  
Pred. No.: 3,12e-144 Length: 2482  
Score: 1163.00 Matches: 205  
Percent Similarity: 99.51% Conservative: 0  
Best Local Similarity: 99.51% Mismatches: 1  
Query Match: 99.66% Indels: 0  
DB: 15 Gaps: 0

US-09-935-390A-23 (1-206) x US-10-245-771-9 (1-2482)

Qy 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
Db 1157 ATGGAAGGCGCCATCCAGTGTCTCTGGCACCCTGTGAGCCACCCAGTTCGGCTGCAGC 1216

Qy 21 AsnGlyCysGlyIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40  
Db 1217 AATGGCTGCTCATCGACAGTTTCTGGAGTGTGACGACACCCCACTGCGCCGACGCC 1276

Qy 41 SerAspGluAlaAlaCysGluIleThrSerGlyPheAspGluLeuGlnArgIleHis 60  
Db 1277 TCCGACGAGGCTGCTGTGAAAATAATACAGAGTGGCTTTGACGAGCTCCAGCGATCCAT 1336

Qy 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
Db 1337 TTCCCAAGTGAAGGCGCACTGCTGGACCTGCGACACACGAGTCTGCAAGGAGAGC 1396

Qy 81 IleProArgTyrTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100  
Db 1397 ATCCCGCGTGTGTACTACACCCCTTACGCGNACACTGCGCCGCTTTACCTATGGTGT 1456

Qy 101 CysTyrGlyAsnLysAsnAsnPheGluGluGluGlnGlnCysLeuGluSerCysArgGly 120  
Db 1457 TGTATATGACACAGACAACTTTGAGGAGAGACAGCAGTGTCTCGAGTCTTGTGCGCGC 1516

Qy 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140  
Db 1517 ATCTCCAGAGAGATGTGTGGCTGTAGGCGGGAAATCCCATTTCCAGACACAGCTCT 1576

Qy 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160  
Db 1577 GTGGAGATGGCTGTACAGATGTTCTGGTCACTGTGCTGTGGTGTAGCCATCTG 1636

Qy 161 GlyTyrCysPhePheLysGlnArgLysAspPheHisGlyHisHisHisProPro 180  
Db 1637 GGTACTGCTCTTCAAGAACCCAGAGAAAGACTTCCCGGACACACACCCACCA 1696

Qy 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200  
Db 1697 CCACCCCTTGGCAGCTTCCACTGTCTCACTACCGAGGACACCGGACCTGCTGTATAAC 1756

Qy 201 HisThrThrArgProLeu 206  
Db 1757 CACACACCGGCCCCCTC 1774

RESULT 13  
US-10-245-851-9  
Sequence 9, Application US/10245851  
Publication No. US20030068782A1  
GENERAL INFORMATION:

APPLICANT: Baker, Kevin  
APPLICANT: Baton, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Phillippe  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C93  
CURRENT APPLICATION NUMBER: US/10/245,851  
CURRENT FILING DATE: 2002-09-16  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/055027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 9  
LENGTH: 2482  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-245-851-9

Alignment Scores:  
Pred. No.: 3,12e-144 Length: 2482  
Score: 1163.00 Matches: 205  
Percent Similarity: 99.51% Conservative: 0  
Best Local Similarity: 99.51% Mismatches: 1  
Query Match: 99.66% Indels: 0  
DB: 15 Gaps: 0

US-09-935-390A-23 (1-206) x US-10-245-851-9 (1-2482)

Qy 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
Db 1157 ATGGAAGGCGCCATCCAGTGTCTCTGGCACCCTGTGAGCCACCCAGTTCGGCTGCAGC 1216

Qy 21 AsnGlyCysGlyIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40  
Db 1217 AATGGCTGCTCATCGACAGTTTCTGGAGTGTGACGACACCCCACTGCGCCGACGCC 1276

Qy 41 SerAspGluAlaAlaCysGluIleThrSerGlyPheAspGluLeuGlnArgIleHis 60  
Db 1277 TCCGACGAGGCTGCTGTGAAAATAATACAGAGTGGCTTTGACGAGCTCCAGCGATCCAT 1336

Qy 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
Db 1337 TTCCCAAGTGAAGGCGCACTGCTGGACCTGCGACACACGAGTCTGCAAGGAGAGC 1396

Qy 81 IleProArgTyrTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100  
Db 1397 ATCCCGCGTGTGTACTACACCCCTTACGCGNACACTGCGCCGCTTTACCTATGGTGT 1456

Qy 101 CysTyrGlyAsnLysAsnAsnPheGluGluGluGlnGlnCysLeuGluSerCysArgGly 120  
Db 1457 TGTATATGACACAGACAACTTTGAGGAGAGACAGCAGTGTCTCGAGTCTTGTGCGCGC 1516

Qy 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140  
Db 1517 ATCTCCAGAGAGATGTGTGGCTGTAGGCGGGAAATCCCATTTCCAGACACAGCTCT 1576

Qy 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160  
Db 1577 GTGGAGATGGCTGTACAGATGTTCTGGTCACTGTGCTGTGGTGTAGCCATCTG 1636

Qy 161 GlyTyrCysPhePheLysGlnArgLysAspPheHisGlyHisHisHisProPro 180  
Db 1637 GGTACTGCTCTTCAAGAACCCAGAGAAAGACTTCCCGGACACACACCCACCA 1696

Qy 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200  
Db 1697 CCACCCCTTGGCAGCTTCCACTGTCTCACTACCGAGGACACCGGACCTGCTGTATAAC 1756

Qy 201 HisThrThrArgProLeu 206  
Db 1757 CACACACCGGCCCCCTC 1774

RESULT 13  
US-10-245-851-9  
Sequence 9, Application US/10245851  
Publication No. US20030068782A1  
GENERAL INFORMATION:

Db 1397 ATCCGCGCTGGTACTACAAACCTTCAGCGAACACTGGCCCGCTTTACCTATGGTGT 1456  
Qy 101 CysThrGlyValAsnLysAsnAsnPhelGluGluGluGlnCysLeuGluSerCysArgGly 120  
Db 1457 TGTATGGCAACAAGAACACTTTGAGGAAGAGCAGCTGCTCGAGTCTTGTGCGGCG 1516  
Qy 121 IleSerLysLysAspValPheGlyLeuArgzGluilleProileProSerThrGlySer 140  
Db 1517 ATCTCCAAAGAGATGTGTTGGCTGAGCGGGAAATCCCAATCCCAAGCACAGGCTCT 1576  
Qy 141 ValGluMetAlaValAlaPheLeuValIleCysIleValValValValAlaIleLeu 160  
Db 1577 GTGGAGATGGCTGTACAGTGTCTCGGTCATCTGCAATGTGGTGTGATGCCATCTG 1636  
Qy 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180  
Db 1637 GGTACTGCTTCTTCAAGAACAGAGAAAGGACTTCCACGGACACCAACCAACCA 1696  
Qy 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200  
Db 1697 CCCACCCCTGCGAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC 1756  
Qy 201 HisThrThrArgProLeu 206  
Db 1757 CACACACCCCGGCCCTC 1774

## RESULT 14

US-10-245-883-9  
; Sequence 9, Application US/10245883  
; Publication No. US20030068783A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3630R1C70  
; CURRENT APPLICATION NUMBER: US/10/245,883  
; PRIOR FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 9  
; LENGTH: 2482  
; TYPE: DNA

; ORGANISM: Homo Sapien  
US-10-245-883-9  
Alignment Scores:  
Pred. No.: 3,12e-144 Length: 2482  
Score: 1163.00 Matches: 205  
Percent Similarity: 99.51% Conservative: 0  
Best Local Similarity: 99.51% Mismatches: 1  
Query Match: 99.66% Indels: 0  
DB: 15 Gaps: 0

US-09-935-390A-23 (1-206) x US-10-245-883-9 (1-2482)

Qy 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
Db 1157 ATGAAAGCGCCATCCAGTGTCTGTGGCACTGTGTGAGCCACCCAGTTCGCTGCGCAGC 1216  
Qy 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspSerThrProAsnCysProAspAla 40  
Db 1217 AATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1276  
Qy 41 SerAspGluAlaAlaCysGluLysThrSerGlyPheAspGluLeuGlnArgIleHis 60  
Db 1277 TCCGAGCAGGCTGCTGTGAAAAATACACGAGTGGCTTTCAGAGCTCCAGCGCATCCAT 1336  
Qy 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
Db 1337 TTCCCCAGTGACAAAGGCACTGGGTGGACCTGCCAGACAGGACTCTGAGAGGAGC 1396  
Qy 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100  
Db 1397 ATCCGCGCTGTACTACACCCCTTCAGCGAACACTGCCGCCGCTTTACCTATGGTGT 1456  
Qy 101 CysTyrGlyAsnLysAsnAsnPhelGluGluGlnCysLeuGluSerCysArgGly 120  
Db 1457 TGTATGGCAACAAGAACACTTTGAGGAAGAGCAGCTGCTCGAGTCTTGTGCGGCG 1516  
Qy 121 IleSerLysLysAspValPheGlyLeuArgzGluilleProileProSerThrGlySer 140  
Db 1517 ATCTCCAAAGAGATGTGTTGGCTGAGCGGGAAATCCCAATCCCAAGCACAGGCTCT 1576  
Qy 141 ValGluMetAlaValAlaPheLeuValIleCysIleValValValValAlaIleLeu 160  
Db 1577 GTGGAGATGGCTGTACAGTGTCTCGGTCATCTGCAATGTGGTGTGATGCCATCTG 1636  
Qy 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180  
Db 1637 GGTACTGCTTCTTCAAGAACAGAGAAAGGACTTCCACGGACACCAACCAACCA 1696  
Qy 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200  
Db 1697 CCCACCCCTGCGAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC 1756  
Qy 201 HisThrThrArgProLeu 206  
Db 1757 CACACACCCCGGCCCTC 1774

## RESULT 15

US-10-237-535-9  
; Sequence 9, Application US/10237535  
; Publication No. US20030073188A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin



APPLICANT: For9.Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C3  
CURRENT FILING DATE: 2002-09-06  
CURRENT APPLICATION NUMBER: US/10/237,535

PRIOR FILING DATE: 1999-08-03  
PRIOR APPLICATION NUMBER: 60/148188  
PRIOR FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: 60/148513  
PRIOR FILING DATE: 1999-08-12  
PRIOR APPLICATION NUMBER: 60/149327  
PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: 60/149395  
PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: 60/150114  
PRIOR FILING DATE: 1999-08-20  
PRIOR APPLICATION NUMBER: 60/151700  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: 60/151734  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: 60/162506  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: 60/170262  
PRIOR FILING DATE: 1999-12-09  
PRIOR APPLICATION NUMBER: 60/177118  
PRIOR FILING DATE: 2000-01-20  
PRIOR APPLICATION NUMBER: 60/179851  
PRIOR FILING DATE: 2000-02-02  
PRIOR APPLICATION NUMBER: 60/180921  
PRIOR FILING DATE: 2000-02-08  
PRIOR APPLICATION NUMBER: 60/187202  
PRIOR FILING DATE: 2000-03-03  
PRIOR APPLICATION NUMBER: 60/198587  
PRIOR FILING DATE: 2000-04-18  
PRIOR APPLICATION NUMBER: 60/199614  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 60/206330  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/206368  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/209832  
PRIOR FILING DATE: 2000-06-05  
PRIOR APPLICATION NUMBER: 60/218371  
PRIOR FILING DATE: 2000-07-13  
PRIOR APPLICATION NUMBER: 60/222695  
PRIOR FILING DATE: 2000-08-02  
PRIOR APPLICATION NUMBER: 60/229896  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/230621  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/232887  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 60/235147  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 60/261878  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: 60/261910  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/261939  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/262150  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/264395  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/266421  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 60/267623  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/274399  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: 60/280982  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/282129  
PRIOR FILING DATE: 2001-04-04  
PRIOR APPLICATION NUMBER: 60/282199  
PRIOR FILING DATE: 2001-04-04  
PRIOR APPLICATION NUMBER: 60/290589  
PRIOR FILING DATE: 2001-05-09

QY	1	MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer	20
DB	1157	ATGGAAGGCGCCATCCAGTGTCTGTGGACCTGTGAGGCCACCCAGTTCGGTGCAGC	1216
QY	21	AsnGlyCysCysIleAspSerPheIeuGluCysAspAspThrProAsnCysProAspAla	40
DB	1217	AATGGTGTCTCATCGACAGTTTCTGTGAGTGTGACGACACCCCCAACTGGCCCCGAGCC	1276
QY	41	SerAspGluAlaIaCysGluLysTyThrSerGlyPheAspGluLeuGlnArgIleHis	60
DB	1277	TCCGAGGAGCGTGCCTGTGAAAAATACAGAGTGGCTTTCAGCAGCTCCAGCGCATCCAT	1336
QY	61	PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer	80
DB	1337	TTCCCCAGTGCACAAAGGCGCACTCGCTGGACCTGGCCAGACACAGGACTCTGCAAGGAGAGC	1396
QY	81	IleProArgGlyTrpTyThrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly	100
DB	1397	ATCCCGCGCGTGATCTACACACCCCTTCAGCGAACACTCGGCCCGCTTTACTCTGTTGGT	1456
QY	101	CysTyTGlyAsnLysAsnAspPheGluGluGlnGlnCysLeuGluSerCysArgGly	120

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 22, 2004, 08:12:09 ; Search time 78 Seconds

(without alignments)  
1465.640 Million cell updates/sec

Title: US-09-935-390A-23

Perfect score: 1167  
Sequence: 1 MERRBPVSGTCQPTQRCR.....TVSTTDETHLVYNTTRPL 206

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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3: /cgn2\_6/ptodata/2/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PTCTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1167	100.0	1542	3	US-08-685-558A-8
2	1167	100.0	1542	4	US-09-765-449-8
3	1167	100.0	1870	3	US-09-071-709-6
C 4	647	55.4	816	3	US-09-020-956-14
C 5	647	55.4	816	3	US-09-030-607-14
C 6	647	55.4	816	4	US-09-439-313-14
C 7	647	55.4	816	4	US-09-352-616A-14
C 8	647	55.4	816	4	US-09-232-149A-14
C 9	647	55.4	816	4	US-09-159-812-14
C 10	647	55.4	816	4	US-09-636-215-14
C 11	647	55.4	816	4	US-09-685-166A-14
C 12	647	55.4	816	4	US-09-115-453-14

C 13	647	55.4	816	4	US-09-688-489-14
C 14	572	49.0	760	3	US-09-020-956-37
C 15	572	49.0	760	3	US-09-030-607-37
C 16	572	49.0	760	4	US-09-439-313-37
C 17	572	49.0	760	4	US-09-352-616A-37
C 18	572	49.0	760	4	US-09-232-149A-37
C 19	572	49.0	760	4	US-09-159-812-37
C 20	572	49.0	760	4	US-09-636-215-37
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C 24	325	27.8	399	3	US-09-312-283C-63
C 25	313	26.8	399	3	US-09-188-930-63
C 26	186	15.9	783	3	US-09-020-956-15
C 27	186	15.9	783	3	US-09-030-607-15
C 28	186	15.9	783	4	US-09-352-616A-15
C 29	186	15.9	783	4	US-09-232-149A-15
C 30	186	15.9	783	4	US-09-159-812-15
C 31	186	15.9	783	4	US-09-636-215-15
C 32	186	15.9	783	4	US-09-685-166A-15
C 33	186	15.9	783	4	US-09-115-453-15
C 34	186	15.9	783	4	US-09-688-489-15
C 35	186	15.9	783	4	US-08-685-660A-4
C 36	173	14.8	759	2	US-08-974-196-4
C 37	173	14.8	759	2	US-08-974-196-4
C 38	173	14.8	1286	4	US-09-016-434-713
C 39	173	14.8	1610	3	US-09-013-896A-1
C 40	173	14.8	1610	4	US-09-827-948-1
C 41	154.5	13.2	979	1	US-08-147-710-1
C 42	154.5	13.2	979	1	US-08-458-080-1
C 43	154.5	13.2	979	2	US-08-457-887-1
C 44	154.5	13.2	979	2	US-09-016-434-1378
C 45	154.5	13.2	979	4	US-09-904-621-1

## ALIGNMENTS

### RESULT 1

US-08-685-558A-8  
Sequence 8, Application US/08685558A  
Patent No. 6225081  
GENERAL INFORMATION:  
APPLICANT: SHIMOMURA, Takeshi  
APPLICANT: KAWAGUCHI, Toshiya  
APPLICANT: KITAMURA, Naomi  
APPLICANT: MIYAZAWA, Keiji  
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME  
TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,558A  
FILING DATE: 24-JUL-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JPA Hei 7-187135  
FILING DATE: 24-JUL-1995  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1542 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA  
 ANTI-SENSE: no  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 STRAIN: MKM45  
 FEATURE:  
 NAME/KEY: coding sequence  
 LOCATION: 1 to 1542  
 IDENTIFICATION METHOD: by experiment  
 NAME/KEY: signal peptide  
 LOCATION: 1 to 105  
 IDENTIFICATION METHOD: by experiment  
 NAME/KEY: mature peptide  
 LOCATION: 106 to 1542  
 IDENTIFICATION METHOD: by experiment

US-08-685-558A-8

Alignment Scores:  
 Pred. No.: 4,596-119 Length: 1542  
 Score: 1167.00 Matches: 206  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

US-09-935-390A-23 (1-206) x US-08-685-558A-8 (1-1542)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
 Db 922 ATGGAAGGCGCATCCAGTGTCTGGCACCCTGTGACCCACCCAGTTCGCGTGCAGC 981  
 QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40  
 Db 982 AATGGCTGTGCATCGACAGTTCCTGGAGTGTGACGACACCCCACTGCCCGACGCC 1041  
 QY 41 SerAspGluAlaAlaCysGluLysThrSerGlyPheAspGluLeuGlnArgIleHis 60  
 Db 1042 TCCGACGAGGCTGCTGTGAATAATACAGAGTGTCTGACGAGCTCCAGCGCATCAT 1101  
 QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
 Db 1102 TTCCCGCAGTGACAAAGGCGCATCTGCTGGACCTGCCAGACACAGGACTCTGCAAGGAGC 1161  
 QY 81 IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrGlyGly 100  
 Db 1162 ATCCCGCGCTGTACTACACCCCTTCAGCAACTGCGCCCGCTTTACCTATGGTGGT 1221  
 QY CysTyrGlyAsnLysAsnAspPheGluGluGlnCysLeuGluSerCysArgGly 120  
 Db 1222 TGTATGTCACACAGAACAACTTTGAGGAGAGGAGCAGTGCCTCGAGTCTGTGGCGGC 1281  
 QY 121 IleSerLysLysAspValPheGlyLeuArgGluIleProIleProSerThrGlySer 140  
 Db 1282 ATCTCCAGAGAGATGTGTTGGCTGAGGCGGGAATCCCATCTCCAGACAGGCTCT 1341  
 QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160  
 Db 1342 GTGGAGATGGCTGTCCAGTGTCTGCTGCTATCTGCTATGCTGTGGTGTGATGCTTG 1401  
 QY 161 GlyTyrCysPhePheLysAsnGlnArgLysPheIleGlyHisHisHisProPro 180  
 Db 1402 GGTACTGCTCTTCAGAACAGAGAAAGGACTTCACGCGACACCAACCCACCA 1461  
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 Db 1462 CCCACCCCTGCCAGTCTCCACTGTCTCCACTACCGAGGACAGGAGCCTGTGCTATAAC 1521  
 QY 201 HisThrThrArgProLeu 206  
 Db 1522 CACACCAACCCGCCCCCTC 1539

RESULT 2

US-09-765-449-8

Sequence 8, Application US/09765449  
 Patent No. 6465622  
 GENERAL INFORMATION:  
 APPLICANT: SHIMOMURA, Takeshi  
 KAWAGUCHI, Toshiya  
 KITAMURA, Naomi  
 MIYAZAWA, Keiji  
 TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME  
 AND METHOD OF PRODUCING THE PROTEIN  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
 STREET: 2100 Pennsylvania Avenue, N.W.  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20037  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy Disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/765,449  
 FILING DATE: 22-Jan-2001  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/685,558  
 FILING DATE: <Unknown>  
 INFORMATION FOR SEQ ID NO: 8  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1542 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 ANTI-SENSE: no  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 STRAIN: MKM45  
 (ix) FEATURES:  
 SEQUENCE DESCRIPTION: SEQ ID NO: 8  
 US-09-765-449-8

Alignment Scores:  
 Pred. No.: 4,596-119 Length: 1542  
 Score: 1167.00 Matches: 206  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 4 Gaps: 0

US-09-935-390A-23 (1-206) x US-09-765-449-8 (1-1542)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
 Db 922 ATGGAAGGCGCATCCAGTGTCTGGCACCCTGTGACCCACCCAGTTCGCGTGCAGC 981  
 QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40  
 Db 982 AATGGCTGTGCATCGACAGTTCCTGGAGTGTGACGACACCCCACTGCCCGACGCC 1041  
 QY 41 SerAspGluAlaAlaCysGluLysThrSerGlyPheAspGluLeuGlnArgIleHis 60  
 Db 1042 TCCGACGAGGCTGCTGTGAATAATACAGAGTGTCTTACGAGCTCCAGCGCATCAT 1101  
 QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
 Db 1102 TTCCCGCAGTGACAAAGGCGCATCTGCTGGACCTGCCAGACACAGGACTCTGCAAGGAGC 1161  
 QY 81 IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrGlyGly 100  
 Db 1162 ATCCCGCGCTGTACTACACCCCTTCAGGAGACACACTGCGCCCGCTTTACCTATGGTGGT 1221



CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-020-956-14
Alignment Scores:
Pred. No.: 3,55e-62 Length: 816
Score: 647.00 Matches: 109
Percent Similarity: 99.10% Conservative: 1
Best Local Similarity: 98.20% Mismatches: 1
Query Match: 55.44% Indels: 0
Gaps: 3
US-09-935-390A-23 (1-206) x US-09-020-956-14 (1-816)
QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 335 ATGGAAGAGCCCATCCAGTGTCTGGACATGTGACGCCACCCAGTTCGGCTGCAGC 276
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
Db 275 AATGGCTGCTGCATNGACAGTTCTCTGGAGTGTGAAGACACCCCAACTGCCCGCAGCG 216
QY 41 SerAspGluAlaAlaCysGluValThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 215 TCGACAGAGGCTGCTGTGAAAATACACAGTGTGCTTACAGAGCTCCAGCGCATCAT 156
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 155 TTCCCCAGTGAACAAGGCACTGGTGGACCTGCCAGACAGGACTCTGCAAGGAGAGC 96
QY 81 IleProArgTrpTyThrAsnProPheSerGluHisCysAlaArgPheThrTyGlyGly 100
Db 95 ATCCCGCGCTGTACTACAAACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGT 36
QY 101 CysTyGlyAsnLysAsnAsnPheGluGlu 111
Db 35 TGTATGSCACACAGAACAACTTTGAGGAAGAG 3
RESULT 5
US-09-030-607-14/c
Sequence 14, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-030-607-14
Alignment Scores:
Pred. No.: 3,55e-62 Length: 816
Score: 647.00 Matches: 109
Percent Similarity: 99.10% Conservative: 1
Best Local Similarity: 98.20% Mismatches: 1
Query Match: 55.44% Indels: 0
Gaps: 3
US-09-935-390A-23 (1-206) x US-09-030-607-14 (1-816)
QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 335 ATGGAAGAGCCCATCCAGTGTCTGGACATGTGACGCCACCCAGTTCGGCTGCAGC 276
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
Db 275 AATGGCTGCTGCATNGACAGTTCTCTGGAGTGTGAAGACACCCCAACTGCCCGCAGCG 216
QY 41 SerAspGluAlaAlaCysGluValThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 215 TCGACAGAGGCTGCTGTGAAAATACACAGTGTGCTTACAGAGCTCCAGCGCATCAT 156
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 155 TTCCCCAGTGAACAAGGCACTGGTGGACCTGCCAGACAGGACTCTGCAAGGAGAGC 96
QY 81 IleProArgTrpTyThrAsnProPheSerGluHisCysAlaArgPheThrTyGlyGly 100
Db 95 ATCCCGCGCTGTACTACAAACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGT 36
QY 101 CysTyGlyAsnLysAsnAsnPheGluGlu 111
Db 35 TGTATGSCACACAGAACAACTTTGAGGAAGAG 3
RESULT 6
US-09-439-313-14/c
Sequence 14, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqi
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C9

; CURRENT APPLICATION NUMBER: US/09/439,313

; CURRENT FILING DATE: 1999-11-12

; NUMBER OF SEQ ID NOS: 575

; SOFTWARE: FASTSEQ for Windows Version 3.0

; SEQ ID NO 14

; LENGTH: 816

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(816)

; OTHER INFORMATION: n = A,T,C or G

US-09-439-313-14

Alignment Scores:  
Pred. No.: 3,55e-62 Length: 816  
Score: 647.00 Matches: 109  
Percent Similarity: 99.10% Conservative: 1  
Best Local Similarity: 98.20% Mismatches: 1  
Query Match: 55.44% Indels: 0  
DB: 4 Gaps: 0

US-09-935-390A-23 (1-206) x US-09-439-313-14 (1-816)

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QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
DB 335 ATGGAAGGGCCATCCAGTGTGCTCTGCACTGTCAGCCACCCAGTTCGGCTGCAGC 276
QY 21 AsnGlyCysCysLeuAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
DB 275 AATGGCTGCTGCATNGACAGTTTCTGGAGTGTGAAGACACCCCACTGCCCGACGG 216
QY 41 SerAspGluAlaAlaCysGluLysThrSerGlyPheAspGluLeuGlnArgIleHis 60
DB 215 TCGGACGAGGCTGCCCTGTGAAAATAACAGAGTGGCTTGACAGCTCCAGGCATCCAT 156
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
DB 155 TTCCCCAGTGACAAAGGGCACTCGGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAG 96
QY 81 IleProArgTrpTyrrAsnProPheSerGluHisCysAlaArgPheThrTyrrGlyGly 100
DB 95 ATCCCGCGCTGGTACTACAAACCCCTTCAGCGAAGACTGGCGCCGCTTACCTATGTGTGT 36
QY 101 CysTyrrGlyAsnLysAsnAsnPheGluGluGlu 111
DB 35 TGTATGGCAACAGACAACTTTGAGGAGAG 3
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RESULT 7

US-09-352-616A-14/c

; Sequence 14, Application US/09352616A

; Patent No. 6395278

; GENERAL INFORMATION:

; APPLICANT: Dillon, Davin C.

; APPLICANT: Harlocker, Susan Louise

; APPLICANT: Jiang, Yuqi

; APPLICANT: Xu, Jiangchun

; APPLICANT: Mitcham, Jennifer Lynn

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

; FILE REFERENCE: 210121.427C8

; CURRENT APPLICATION NUMBER: US/09/352,616A

; CURRENT FILING DATE: 1999-07-13

; NUMBER OF SEQ ID NOS: 472

; SOFTWARE: FASTSEQ for Windows Version 3.0

; SEQ ID NO 14

; LENGTH: 816

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(816)

; OTHER INFORMATION: n = A,T,C or G

US-09-232-149A-14

Alignment Scores:  
Pred. No.: 3,55e-62 Length: 816  
Score: 647.00 Matches: 109  
Percent Similarity: 99.10% Conservative: 1  
Best Local Similarity: 98.20% Mismatches: 1  
Query Match: 55.44% Indels: 0  
DB: 4 Gaps: 0

US-09-935-390A-23 (1-206) x US-09-232-149A-14 (1-816)

; LOCATION: (1)...(816)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-352-616A-14

Alignment Scores:

Pred. No.: 3,55e-62 Length: 816  
Score: 647.00 Matches: 109  
Percent Similarity: 99.10% Conservative: 1  
Best Local Similarity: 98.20% Mismatches: 1  
Query Match: 55.44% Indels: 0  
DB: 4 Gaps: 0

US-09-935-390A-23 (1-206) x US-09-352-616A-14 (1-816)

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QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
DB 335 ATGGAAGGGCCATCCAGTGTGCTCTGCACTGTCAGCCACCCAGTTCGGCTGCAGC 276
QY 21 AsnGlyCysCysLeuAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
DB 275 AATGGCTGCTGCATNGACAGTTTCTGGAGTGTGAAGACACCCCACTGCCCGACGG 216
QY 41 SerAspGluAlaAlaCysGluLysThrSerGlyPheAspGluLeuGlnArgIleHis 60
DB 215 TCGGACGAGGCTGCCCTGTGAAAATAACAGAGTGGCTTGACAGCTCCAGGCATCCAT 156
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
DB 155 TTCCCCAGTGACAAAGGGCACTCGGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAG 96
QY 81 IleProArgTrpTyrrAsnProPheSerGluHisCysAlaArgPheThrTyrrGlyGly 100
DB 95 ATCCCGCGCTGGTACTACAAACCCCTTCAGCGAAGACTGGCGCCGCTTACCTATGTGTGT 36
QY 101 CysTyrrGlyAsnLysAsnAsnPheGluGluGlu 111
DB 35 TGTATGGCAACAGACAACTTTGAGGAGAG 3
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RESULT 8

US-09-232-149A-14/c

; Sequence 14, Application US/09232149A

; Patent No. 6465611

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer Lynn

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

; FILE REFERENCE: 210121.427C6

; CURRENT APPLICATION NUMBER: US/09/232,149A

; CURRENT FILING DATE: 1999-01-15

; NUMBER OF SEQ ID NOS: 338

; SOFTWARE: FASTSEQ for Windows Version 3.0

; SEQ ID NO 14

; LENGTH: 816

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(816)

; OTHER INFORMATION: n = A,T,C or G

US-09-232-149A-14

Alignment Scores:  
Pred. No.: 3,55e-62 Length: 816  
Score: 647.00 Matches: 109  
Percent Similarity: 99.10% Conservative: 1  
Best Local Similarity: 98.20% Mismatches: 1  
Query Match: 55.44% Indels: 0  
DB: 4 Gaps: 0

US-09-935-390A-23 (1-206) x US-09-232-149A-14 (1-816)

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QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
DB 335 ATGAAAGGGCCATCCAGTGTCTCTGGACATGTTCAGCCACCCAGTTCCGCTGCAGC 276

QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
DB 275 AATGGCTGCTGCATNGACAGTTCTCTGGAGTGTGAACACACCCCACTGCCCGAGCG 216

QY 41 SerAspGluAlaAlaCysGluLysTyThrSerGlyPheAspGluLeuGlnArgIleHis 60
DB 215 TCGGACGAGGCTGCTGTGAAATAATACACAGTGGCTTTGACGAGCTCCAGCGCATCAT 156

QY 61 PheProSerAspGlyGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
DB 155 TTCCCCAGTGAACAAAGGGCACTGCTGGACCTGCCAGACACGAGACTTCGACGAGAGC 96

QY 81 IleProArgTyrTyThrAsnProPheSerGluHisCysAlaArgPheThrTyrglyGly 100
DB 95 ATCCCGGCTGTACTACACCCCTTCAGCGAACACTGCGCGCGCTTTACCTATGTGTGT 36

QY 101 CysTyrglyAsnLysAsnAsnPheGluGluGlu 111
DB 35 TGTTATGGCAACAAGAACAACTTTGAGGAAGAG 3

RESULT 9
US-09-812-14/c
; Sequence 14, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C5
; CURRENT APPLICATION NUMBER: US/09/159,812A
; CURRENT FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(816)
; OTHER INFORMATION: n = A,T,C or G
US-09-159-812-14

Alignment Scores:
Pred. No.: 3,55e-62 Length: 816
Score: 647.00 Matches: 109
Percent Similarity: 99.10% Conservative: 1
Best Local Similarity: 98.20% Mismatches: 1
Query Match: 55.44% Indels: 0
DB: 4 Gaps: 0

US-09-935-390A-23 (1-206) x US-09-159-812-14 (1-816)
QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
DB 335 ATGAAAGGGCCATCCAGTGTCTCTGGACATGTTCAGCCACCCAGTTCCGCTGCAGC 276

QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
DB 275 AATGGCTGCTGCATNGACAGTTCTCTGGAGTGTGAACACACCCCACTGCCCGAGCG 216

QY 41 SerAspGluAlaAlaCysGluLysTyThrSerGlyPheAspGluLeuGlnArgIleHis 60
DB 215 TCGGACGAGGCTGCTGTGAAATAATACACAGTGGCTTTGACGAGCTCCAGCGCATCAT 156

QY 61 PheProSerAspGlyGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
DB 155 TTCCCCAGTGAACAAAGGGCACTGCTGGACCTGCCAGACACGAGACTTCGACGAGAGC 96

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QY 81 IleProArgTyrTyThrAsnProPheSerGluHisCysAlaArgPheThrTyrglyGly 100
DB 95 ATCCCGGCTGTACTACACCCCTTCAGCGAACACTGCGCGCGCTTTACCTATGTGTGT 36

QY 101 CysTyrglyAsnLysAsnAsnPheGluGluGlu 111
DB 35 TGTTATGGCAACAAGAACAACTTTGAGGAAGAG 3

RESULT 10
US-09-636-215-14/c
; Sequence 14, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlock, Jennifer L.
; APPLICANT: Harlock, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Ronger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(816)
; OTHER INFORMATION: n = A,T,C or G
US-09-636-215-14

Alignment Scores:
Pred. No.: 3,55e-62 Length: 816
Score: 647.00 Matches: 109
Percent Similarity: 99.10% Conservative: 1
Best Local Similarity: 98.20% Mismatches: 1
Query Match: 55.44% Indels: 0
DB: 4 Gaps: 0

US-09-935-390A-23 (1-206) x US-09-636-215-14 (1-816)
QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
DB 335 ATGAAAGGGCCATCCAGTGTCTCTGGACATGTTCAGCCACCCAGTTCCGCTGCAGC 276

QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
DB 275 AATGGCTGCTGCATNGACAGTTCTCTGGAGTGTGAACACACCCCACTGCCCGAGCG 216

QY 41 SerAspGluAlaAlaCysGluLysTyThrSerGlyPheAspGluLeuGlnArgIleHis 60
DB 215 TCGGACGAGGCTGCTGTGAAATAATACACAGTGGCTTTGACGAGCTCCAGCGCATCAT 156

QY 61 PheProSerAspGlyGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
DB 155 TTCCCCAGTGAACAAAGGGCACTGCTGGACCTGCCAGACACGAGACTTCGACGAGAGC 96

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Qy 81 IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100  
Db 95 ATCCCGCGCTGGTACTACACCCCTTCAGCGAACACTGGCGCCGCTTTACCTATGTGT 36

Qy 101 CysTyrGlyAsnLysAsnAsnPheGluGlu 111  
Db 35 TGTATGGCAACAAGAACAACTTTGAGGAAGAG 3

RESULT 11  
US-09-685-166A-14/c  
; Sequence 14, Application US/09685166A  
; Patent No. 6630305  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C21  
; CURRENT APPLICATION NUMBER: US/09/685,166A  
; CURRENT FILING DATE: 2000-10-10  
; NUMBER OF SEQ ID NOS: 898  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 816  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(816)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-685-166A-14

Alignment Scores:  
Pred. No.: 3,55e-62 Length: 816  
Score: 647.00 Matches: 109  
Percent Similarity: 99.10% Conservative: 1  
Best Local Similarity: 98.20% Mismatches: 1  
Query Match: 55.44% Indels: 0  
DB: 4 Gaps: 0

US-09-935-390A-23 (1-206) x US-09-685-166A-14 (1-816)

Qy 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
Db 335 ATGGAAGGCGCCATCCAGTGTCTTGGCACTGTGAGCCACCCAGTTCGCTGCAGC 276

Qy 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40  
Db 275 AATGGCTGCTGCATNGACAGTTTCTTGGAGTGTGAAGACACCCCACTGCCCGCAGCG 216

Qy 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60  
Db 215 TCGGACGAGGCTGCCTGTGAAAAATACAGAGTGGCTTTGACGAGCTCCAGGCGCATCCAT 156

Qy 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
Db 155 TTCCCGAGTGCACAAAGGCGCACTTCTGGACCTGGACCTGCAGACACAGGACTCTGCAAGGAGAGC 96

Qy 81 IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100  
Db 95 ATCCCGCGCTGGTACTACACCCCTTCAGCGAACACTGGCGCCGCTTTACCTATGTGT 36

Qy 101 CysTyrGlyAsnLysAsnAsnPheGluGlu 111  
Db 35 TGTATGGCAACAAGAACAACTTTGAGGAAGAG 3

RESULT 13  
US-09-688-489-14/c  
; Sequence 14, Application US/09688489  
; Patent No. 6664377  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun

Qy 81 IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100  
Db 95 ATCCCGCGCTGGTACTACACCCCTTCAGCGAACACTGGCGCCGCTTTACCTATGTGT 36

Qy 101 CysTyrGlyAsnLysAsnAsnPheGluGlu 111  
Db 35 TGTATGGCAACAAGAACAACTTTGAGGAAGAG 3

RESULT 12  
US-09-115-453-14/c  
; Sequence 14, Application US/09115453B  
; Patent No. 6657056  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND  
; TITLE OF INVENTION: METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.427C4  
; CURRENT APPLICATION NUMBER: US/09/115,453B  
; CURRENT FILING DATE: 1998-07-14  
; NUMBER OF SEQ ID NOS: 228  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 816  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(816)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-115-453-14

Alignment Scores:  
Pred. No.: 3,55e-62 Length: 816  
Score: 647.00 Matches: 109  
Percent Similarity: 99.10% Conservative: 1  
Best Local Similarity: 98.20% Mismatches: 1  
Query Match: 55.44% Indels: 0  
DB: 4 Gaps: 0

US-09-935-390A-23 (1-206) x US-09-115-453-14 (1-816)

Qy 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20  
Db 335 ATGGAAGGCGCCATCCAGTGTCTTGGCACTGTGAGCCACCCAGTTCGCTGCAGC 276

Qy 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40  
Db 275 AATGGCTGCTGCATNGACAGTTTCTTGGAGTGTGAAGACACCCCACTGCCCGCAGCG 216

Qy 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60  
Db 215 TCGGACGAGGCTGCCTGTGAAAAATACAGAGTGGCTTTGACGAGCTCCAGGCGCATCCAT 156

Qy 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80  
Db 155 TTCCCGAGTGCACAAAGGCGCACTTCTGGACCTGGACCTGCAGACACAGGACTCTGCAAGGAGAGC 96

Qy 81 IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100  
Db 95 ATCCCGCGCTGGTACTACACCCCTTCAGCGAACACTGGCGCCGCTTTACCTATGTGT 36

Qy 101 CysTyrGlyAsnLysAsnAsnPheGluGlu 111  
Db 35 TGTATGGCAACAAGAACAACTTTGAGGAAGAG 3

RESULT 13  
US-09-688-489-14/c  
; Sequence 14, Application US/09688489  
; Patent No. 6664377  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun

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SOFTWARE: PatentIn Release #1.0, Version #1.3.3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO.: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-020-956-37

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	Alignment Scores:	
Pred. No.:	5.85e-54	Length:
Score:	572.00	Matches:
Percent Similarity:	92.93%	Conservative:
Best Local Similarity:	91.15%	Mismatches:
Query Match:	49.01%	Indels:
DR:	3	Gaps:
		760

Qy	1	MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer	20
Db	335	ATGGAAGGGCGCCATCCAGTGTGCTCTGGCACTGTGAGCCACCCAGTTCGCGTCGAGC	276
Qy	21	AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla	40
Db	275	AATGCTGCTGCAATNGACAGTTTCTGGATGTGGAGACACCCCACTGCCCGCCGCGG	216
Qy	41	SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis	60
Db	215	TGGCAGCAGGCTCGCTGTGAAAAATACACGAGTGGCTTTTGACGAGCTCCAGCGCATCCAT	156
Qy	61	PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer	80
Db	155	TTCCCCAGTGACAAAGGGCACTGGCGTGACCTGCCAGACACAGGACTCTGCAAGGAGAC	96
Qy	81	IleProArgTyrTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly	100
Db	95	ATCCCGCGCTGGTACTACAAACCCCTTCAGCGAAACACTGCGCGCGCTTTACTATGTGGT	36
Qy	101	CysTyrGlyValnLysAsnAsnPheGluGlu	111
Db	35	TGTTATGGCAACAAGAACAACTTTGAGGAAG	3

US-09-020-956-37/c  
; Sequence 37, Application US/09020956

Sequence 37, Application 08/05020938  
Patent No. 6261562  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillin, Davin C.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR  
NUMBER OF SEQUENCES: 178  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

US-09-030-607-37/c

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: Sequence 37, Application US/09030607
: Patent No. 6262245
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR
: NUMBER OF SEQUENCES: 224
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SEED and BERRY LLP
: STREET: 6300 Columbia Center, 701 Fifth Avenue
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

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/ COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Patent In Release #1.0, Version #1.30  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/09/030,607  
 / FILING DATE: 25-FEB-1998  
 / CLASSIFICATION:  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Maki, David J.  
 / REGISTRATION NUMBER: 31,392  
 / REFERENCE/DOCKET NUMBER: 210121.427C3  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: (206) 622-4900  
 / TELEFAX: (206) 682-6031  
 / INFORMATION FOR SEQ ID NO: 37:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 760 base pairs  
 / TYPE: nucleic acid  
 / STRANDEDNESS: single  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: cDNA  
 / US-09-030-607-37

Alignment Scores:  
 Pred. No.: 5,85e-54 Length: 760  
 Score: 572.00 Matches: 103  
 Percent Similarity: 92.92% Conservative: 2  
 Best Local Similarity: 91.15% Mismatches: 7  
 Query Match: 49.01% Indels: 2  
 DB: 3 Gaps: 0

US-09-935-390A-23 (1-206) x US-09-030-607-37 (1-760)

QY	1	MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer	20
DB	341	ATGGAAGGCC-NATCCAGTGTTCTGGCACCCTGTGACCCACCCCGTTCGCTCCAGC	283
QY	21	AsnGlyCys-CysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAl	40
DB	282	ATGGGCTGNTGATCGACAGTTTAGTGAGTGTGACGACACCCCACTGCCCGGANGC	223
QY	40	aSerAspGluAlaAlaCysGluLysThrSerGlyPheAspGluLeuGlnArgIleHi	60
DB	222	TTCCGAGGAGGCTGCTGTGAAAAATACACGAGTGGTTNGACGACTCCAGCGCATCCA	163
QY	60	sPheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSe	80
DB	162	TTTCCCAAGTGCACAAAGGGCATTTGCTGGACCTGCCAGACACAGGACTCTGCAAGAGAG	103
QY	80	rIleProArgTTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGl	100
DB	102	CATCCCGCGCTGGTACTACAAACCCCTTCAGCGAACACTGCGCCGCTTTACCTATGCTGG	43
QY	100	yCysTyrGlyAsnLysAsnAsnPheGluGluGln	112
DB	42	TTGTTATGGCAACAGAACAACTTTGAGGAAGAGCAG	6

Search completed: April 22, 2004, 10:15:22  
 Job time : 82 secs



QY 9 CACGAGGAGCAGATCTCTCAAGAGTTTCGTTATGAGGCTGCTTGGGCAACAAC 68  
DB 396 CCACAGGAGCAGATCTCTCAAGAGTTTCGTTATGAGGCTGCTTGGGCAACAAC 457  
QY 69 TACCTTCGGGAGAGAGTGCATTCWAGCTCTGCGGGGTGTGCAAGTGGGCTTTGAGA 128  
DB 458 TACCTTCGGGAGAGAGTGCATTCWAGCTCTGCGGGGTGTGCAAGTGGGCTTTGAGA 517  
QY 129 GGCAGCTCTGGGCTCAGGCGACTTTCCTCCAGGCGCTTCCATGGAAAGCGCCATCCA 188  
DB 518 GGCAGCTCTGGGCTCAGGCGACTTTCCTCCAGGCGCTTCCATGGAAAGCGCCATCCA 577  
QY 189 GTGTGCTCTGGCACTCTGACGCCACCCAGTTCGGTGCAGCAATGCTCTGCATGCAC 248  
DB 578 GTGTGCTCTGGCACTCTGACGCCACCCAGTTCGGTGCAGCAATGCTCTGCATGCAC 637  
QY 249 AGTTTCTGTGAGTGTGACGACACCCCACTGCGCCCGACGCTCCGACGAGGCTGCTGT 308  
DB 638 AGTTTCTGTGAGTGTGACGACACCCCACTGCGCCCGACGCTCCGACGAGGCTGCTGT 697  
QY 309 GAAATAATACAGAGTGGCTTTGACGAGCTCCAGCGCATTCATTTCCAGCGCAAAAGGG 368  
DB 698 GAAATAATACAGAGTGGCTTTGACGAGCTCCAGCGCATTCATTTCCAGCGCAAAAGGG 757  
QY 369 CACTGCGTGGACCTGCGACACAGGACTCTGCAAGAGAGCATCCCGCTGCTACTAC 428  
DB 758 CACTGCGTGGACCTGCGACACAGGACTCTGCAAGAGAGCATCCCGCTGCTACTAC 817  
QY 429 AACCCCTTCAGCAACTGCGCGCGCTTTACCTATGCTGTGTTTACGGCAACAAGAAC 488  
DB 818 AACCCCTTCAGCAACTGCGCGCGCTTTACCTATGCTGTGTTTACGGCAACAAGAAC 877  
QY 489 AACTTTGAGGAGAGCAGAGTGGCTGTGAGTCTTGTGCGGCATCTCCAGAGGATGTG 548  
DB 878 AACTTTGAGGAGAGCAGAGTGGCTGTGAGTCTTGTGCGGCATCTCCAGAGGATGTG 937  
QY 549 TTTGCGCTGAGCGGGAATCCCATTCAGCAGCAGGCTCTGTGGAGATGGCTGTGCGCA 608  
DB 938 TTTGCGCTGAGCGGGAATCCCATTCAGCAGCAGGCTCTGTGGAGATGGCTGTGCGCA 997  
QY 609 GTGTTCCTGTCATCTGCAATGTGGTGTGAGTGTGAGTCTTTGGGTACTGCTTCTCAAG 669  
DB 998 GTGTTCCTGTCATCTGCAATGTGGTGTGAGTGTGAGTCTTTGGGTACTGCTTCTCAAG 1057  
QY 669 AACGAGAGAGAGGACTTCCAGGACACACACACACACACACACACACACACACACAC 728  
DB 1058 AACGAGAGAGAGGACTTCCAGGACACACACACACACACACACACACACACACACAC 1117  
QY 729 ACTGTCTCCACTACCGAGGACACGAGCACTGTGCTATATACCAACACACACACACAC 788  
DB 1118 ACTGTCTCCACTACCGAGGACACGAGCACTGTGCTATATACCAACACACACACACAC 1177  
QY 789 TGAGCTGGGTCTCACCGGCTCTACCTGGCGCTGCTTCCCTGCTTCCAGGAGAGGCC 848  
DB 1178 TGAGCTGGGTCTCACCGGCTCTACCTGGCGCTGCTTCCCTGCTTCCAGGAGAGGCC 1237  
QY 849 TGGGCTGGGAAATACTTTGGAAACAGACTCTTGGCTGTTCCTCCAGGCGCCACTGTGCTCA 908  
DB 1238 TGGGCTGGGAAATACTTTGGAAACAGACTCTTGGCTGTTCCTCCAGGCGCCACTGTGCTCA 1297  
QY 909 GAGACACAGGCTCCAGCGCTCTTGGAGAGTCTCAGCTAGCTCAGCTCTGAGAAAGC 968  
DB 1298 GAGACACAGGCTCCAGCGCTCTTGGAGAGTCTCAGCTAGCTCAGCTCTGAGAAAGC 1357  
QY 969 TCAAGAGTTTGAAGGAGCAGAAACCTTTGGGCGAGAGTACACAGCTAGATGAGCCTG 1028  
DB 1358 TCAAGAGTTTGAAGGAGCAGAAACCTTTGGGCGAGAGTACACAGCTAGATGAGCCTG 1417  
QY 1029 CCTGCATAGAGTTTGGAGAGTGTGAGTTTGTCTCTGTTTCAAGCTGCTGTCC 1088  
DB 1418 CCTGCATAGAGTTTGGAGAGTGTGAGTTTGTCTCTGTTTCAAGCTGCTGTCC 1477

## RESULT 2

US-08-685-558A-8  
; Sequence 8, Application US/08685558A  
; Patent No. 6225081  
; GENERAL INFORMATION:  
; APPLICANT: SHIMOMURA, Takeshi  
; APPLICANT: KAWAGUCHI, Toshiya  
; APPLICANT: KITAMURA, Naomi  
; APPLICANT: MIYAZAWA, Keiji  
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME  
; TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SUGHRUE, MILO, ZINN, MACPHEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685,558A  
; FILING DATE: 24-JUL-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JPA Hei 7-187135  
; FILING DATE: 24-JUL-1995  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1542 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; ANTI-SENSE: no  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; STRAIN: MN45  
; FEATURE:  
; NAME/KEY: coding sequence  
; LOCATION: 1 to 1542

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/ IDENTIFICATION METHOD: by experiment
/ NAME/KEY: signal peptide
/ LOCATION: 1 to 105
/ IDENTIFICATION METHOD: by experiment
/ NAME/KEY: mature peptide
/ LOCATION: 106 to 1542
/ IDENTIFICATION METHOD: by experiment
; US-08-685-558A-8

Query Match      44.3%; Score 667.4; DB 3; Length 1542;
Best Local Similarity 93.1%; Pred. No. 3.3e-168;
Matches 729; Conservative 0; Mismatches 6; Indels 48; Gaps 1;

QY 9 CACGAGGAGCAGATCTGCAAGAGTTCGTTATGAGGCTGCTTGGCAACAGAAC 68
DB 808 CCACGAGGAGATCTGCAAGAGTTCGTTATGAGGCTGCTTGGCAACAGAAC 867

QY 69 TACCTTCGGGAAGAGAGTTCATTTAGCCTGTGCGGGGTGTGCAAGGTGGGCTTTGAGA 128
DB 868 TACCTTCGGGAAGAGAGTTCATTTAGCCTGTGCGGGGTGTGCAAGGTGGGCTTTGAGA 912

QY 129 GGCAGCTCTGGGCTCAGGCGACTTTCGCCAGGGGCCCTCCATGGAAGGCGCCATCCA 188
DB 913 -----GGCCCCCTCCATGGAAGGCGCCATCCA 939

QY 189 GTGTGCTCTGCGACCTGTGAGCCACCCAGTTCGCTGAGCAATGGCTGTCATCGAC 248
DB 940 GTGTGCTCTGCGACCTGTGAGCCACCCAGTTCGCTGAGCAATGGCTGTCATCGAC 999

QY 249 AGTTTCTCGAGTGTGACGACACCCCACTGCCCCGAGCGCTCCGACGAGGCTGCTGT 308
DB 1000 AGTTTCTCGAGTGTGACGACACCCCACTGCCCCGAGCGCTCCGACGAGGCTGCTGT 1059

QY 129 GGCAGCTCTGGGCTCAGGCGACTTTCGCCAGGGGCCCTCCATGGAAGGCGCCATCCA 188
DB 913 -----GGCCCCCTCCATGGAAGGCGCCATCCA 939

QY 189 GTGTGCTCTGCGACCTGTGAGCCACCCAGTTCGCTGAGCAATGGCTGTCATCGAC 248
DB 940 GTGTGCTCTGCGACCTGTGAGCCACCCAGTTCGCTGAGCAATGGCTGTCATCGAC 999

QY 249 AGTTTCTCGAGTGTGACGACACCCCACTGCCCCGAGCGCTCCGACGAGGCTGCTGT 308
DB 1000 AGTTTCTCGAGTGTGACGACACCCCACTGCCCCGAGCGCTCCGACGAGGCTGCTGT 1059

QY 309 GAAAAATACACGAGTGTGACGACACCCCACTGCCCCGAGCGCTCCGACGAGGCTGCTGT 368
DB 1060 GAAAAATACACGAGTGTGACGACACCCCACTGCCCCGAGCGCTCCGACGAGGCTGCTGT 1119

QY 369 CACTGCGTGTGACCTGCGAGACACAGGACTCTGCAAGGAGAGCATCCGCGCTGTACTAC 428
DB 1120 CACTGCGTGTGACCTGCGAGACACAGGACTCTGCAAGGAGAGCATCCGCGCTGTACTAC 1179

QY 429 AACCCCTTCAGCGAAGAGTGTGAGCTGCTGAGCTGCTGAGCTGCTGAGCTGCTGAGCT 488
DB 1180 AACCCCTTCAGCGAAGAGTGTGAGCTGCTGAGCTGCTGAGCTGCTGAGCTGCTGAGCT 1239

QY 489 AACTTTGAGGAGAGAGAGTGTGAGCTGCTGAGCTGCTGAGCTGCTGAGCTGCTGAGCT 548
DB 1240 AACTTTGAGGAGAGAGAGTGTGAGCTGCTGAGCTGCTGAGCTGCTGAGCTGCTGAGCT 1299

QY 549 TTTGGCTGTGAGCGGGAAATCCCATTCGAGCAAGGCTCTGAGGAGATGGCTGTGCGCA 608
DB 1300 TTTGGCTGTGAGCGGGAAATCCCATTCGAGCAAGGCTCTGAGGAGATGGCTGTGCGCA 1359

QY 609 GTGTTCCTGTGTCATCTGATGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 668
DB 1360 GTGTTCCTGTGTCATCTGATGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1419

QY 669 AACGAGAGAAAGGACTTCCAGGACACCAACCAACCAACCAACCAACCAACCAACCAACCA 728
DB 1420 AACGAGAGAAAGGACTTCCAGGACACCAACCAACCAACCAACCAACCAACCAACCAACCA 1479

QY 729 ACTGTCTCCATGAGGAGGACAGGAGCACTGTGTATACACACACACACACACACACACAC 788
DB 1480 ACTGTCTCCATGAGGAGGACAGGAGCACTGTGTATACACACACACACACACACACACAC 1539

QY 789 TGA 791
DB 1540 TGA 1542
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RESULT 3
US-09-765-449-8
; Sequence 8, Application US/09765449
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/ Patent No. 6465622
/ GENERAL INFORMATION:
/ APPLICANT: SHIMOMURA, Takeshi
/ KAWAGUCHI, Toshiya
/ KITAMURA, Naomi
/ MIYAZAWA, Keiji
/ TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
/ AND METHOD OF PRODUCING THE PROTEIN
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SUGHRUE, MION, ZINN, MACPHEAK & SEAS
/ STREET: 2100 Pennsylvania Avenue, N.W.
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20037
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy Disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/765,449
/ FILING DATE: 22-Jan-2001
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/685,558
/ FILING DATE: <Unknown>
/ INFORMATION FOR SEQ ID NO: 8
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1542 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ ANTI-SENSE: no
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ STRAIN: MN45
/ SEQUENCE DESCRIPTION: SEQ ID NO: 8
US-09-765-449-8
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Query Match      44.3%; Score 667.4; DB 4; Length 1542;
Best Local Similarity 93.1%; Pred. No. 3.3e-168;
Matches 729; Conservative 0; Mismatches 6; Indels 48; Gaps 1;

QY 9 CACGAGGAGCAGATCTGCAAGAGTTCGTTATGAGGCTGCTTGGCAACAGAAC 68
DB 808 CCACGAGGAGATCTGCAAGAGTTCGTTATGAGGCTGCTTGGCAACAGAAC 867

QY 69 TACCTTCGGGAAGAGAGTTCATTTAGCCTGTGCGGGGTGTGCAAGGTGGGCTTTGAGA 128
DB 868 TACCTTCGGGAAGAGAGTTCATTTAGCCTGTGCGGGGTGTGCAAGGTGGGCTTTGAGA 912

QY 129 GGCAGCTCTGGGCTCAGGCGACTTTCGCCAGGGGCCCTCCATGGAAGGCGCCATCCA 188
DB 913 -----GGCCCCCTCCATGGAAGGCGCCATCCA 939

QY 189 GTGTGCTCTGCGACCTGTGAGCCACCCAGTTCGCTGAGCAATGGCTGTCATCGAC 248
DB 940 GTGTGCTCTGCGACCTGTGAGCCACCCAGTTCGCTGAGCAATGGCTGTCATCGAC 999

QY 249 AGTTTCTCGAGTGTGACGACACCCCACTGCCCCGAGCGCTCCGACGAGGCTGCTGT 308
DB 1000 AGTTTCTCGAGTGTGACGACACCCCACTGCCCCGAGCGCTCCGACGAGGCTGCTGT 1059

QY 309 GAAAAATACACGAGTGTGACGACACCCCACTGCCCCGAGCGCTCCGACGAGGCTGCTGT 368
DB 1060 GAAAAATACACGAGTGTGACGACACCCCACTGCCCCGAGCGCTCCGACGAGGCTGCTGT 1119

QY 369 CACTGCGTGTGACCTGCGAGACACAGGACTCTGCAAGGAGAGCATCCGCGCTGTACTAC 428
DB 1120 CACTGCGTGTGACCTGCGAGACACAGGACTCTGCAAGGAGAGCATCCGCGCTGTACTAC 1179
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Qy	429	AACCCCTTCAGCGAACACTGGGCGCGCTTTACCTATGGTGGTGTGTACGGCAACAGAAAC	488
Db	1180	AACCCCTTCAGCGAACACTGGGCGCGCTTTACCTATGGTGGTGTGTATGSCAACAGAAAC	1239
Qy	489	AACCTTTGAGGAAGACAGCAGTGCCTCGAGTCTTGTCCGGCATCTCCAGAAGGATGTG	548
Db	1240	AACCTTTGAGGAAGACAGCAGTGCCTCGAGTCTTGTCCGGCATCTCCAGAAGGATGTG	1299
Qy	549	TTTGGCCTGAGCGGGGAAATCCCAATCCAGCACAGGCTCTGTGGAGATGGCTGTGCGCA	608
Db	1300	TTTGGCCTGAGCGGGGAAATCCCAATCCAGCACAGGCTCTGTGGAGATGGCTGTGCGCA	1359
Qy	609	GTGTTCTCTGTCATCTGCAATGTGTGGTGGTAGCCATCTTGGGTACTGCTTCTCAAG	668
Db	1360	GTGTTCTCTGTCATCTGCAATGTGTGGTGGTAGCCATCTTGGGTACTGCTTCTCAAG	1419
Qy	669	AACCAAGAAGAAGACTTCCAGGAGACACACACACCCACACCCCTGCGCAGTCC	728
Db	1420	AACCAAGAAGAAGACTTCCAGGAGACACACACACCCACACCCCTGCGCAGTCC	1479
Qy	729	ACTGTCTTCCACTACCGAGGACAGGAGCACTGGTCTATACCAACACACCGCGGCCCTC	788
Db	1480	ACTGTCTTCCACTACCGAGGACAGGAGCACTGGTCTATACCAACACACCGCGGCCCTC	1539
Qy	789	TGA 791	
Db	1540	TGA 1542	

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RESULT 4
US-09-020-956-14/c
; Sequence 14, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillin, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and HERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 816 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-020-956-14
Query Match 27.5%; Score 413.4; DB 3; Length 816;
Best Local Similarity 92.0%; Pred. No. 1.3e-100;

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Matches 459; Conservative 0; Mismatches 37; Indels 3; Gaps 3

QY 9 CACGAGGAGCAGATCTCGCAAGAGTTTGTTTATGGAGGCTGCTTGGGCAACAAGAACAC 68  
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Db 498 CCNCGCGAGCAGATATGCAAGAGTTT-GTTTANGGGGNTGGNTGGGCAACAAGAAAC 440  
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QY 69 TACC-TTCGGGAGAGAGAGTGCAATCTAGCCTCTCGGGGTGTCAGGT-GGGGCTTTGA 126  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 439 TACCTTTGCGGAAGAGAGATTCATTTCTAGCCTCTTCGGGGTGTGCLAGGTGGGGNTTTGA 380  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 127 GAGCGACGCTCTGGGGCTCAGGCGCACTTTCCCCCAGGGCCCCCTCCATGGAAAGGCGCCATC 186  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 379 GAGCGAGNTTNGGGGNTCAGGGACTTTCCNCAGGGGCCNTNNCATGGAAAGGCGCCATC 320  
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QY 187 CAGTGTGCTCTGGCACTGTTCAGGCCACCCAGTTCCGCTGCAGCAATGGCTGTGCATCG 246  
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Db 319 CAGTGTGCTCTGGCAGTGTTCAGGCCACCCAGTTCCGCTGCAGCAATGGCTGTGCATCG 260  
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QY 247 ACAGTTTCTCGGAGTGTGACGACACCCCACTGCCCCCGAGCGCTCCGACGAGGCTGCT 306  
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Db 259 ACAGTTTCTCGGAGTGTGAGACACCCCACTGCCCCCGAGCGCTCCGACGAGGCTGCT 200  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 307 GTGAAATAACAGAGTGGCTTTGACGAGCTCCAGGCGCTCCATTTCCCGAGCGACCAAG 366  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 199 GTGAAATAACAGAGTGGCTTTGACGAGCTCCAGGCGCTCCATTTCCCGAGCGACCAAG 140  
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QY 367 GGCACCTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACT 426  
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Db 139 GGCACCTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACT 80  
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QY 427 ACAACCCCTTCGCGAACAACCTGCGCGCTTTACCTATGTTGGTGTGTTCGCGACACAGA 486  
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Db 79 ACAACCCCTTCGCGAACAACCTGCGCGCTTTACCTATGTTGGTGTGTTCGCGACACAGA 20  
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QY 487 ACAACTTGGAGGAGAGCA 505  
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Db 19 ACAACTTGGAGGAGAGCA 1

RESULT 5  
US-09-030-607-14/c  
; Sequence 14, Application US/09030607  
; Patent No. 6262245  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Devin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND ME  
; NUMBER OF SEQUENCES: 224  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,607  
; FILING DATE: 25-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.427C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4500  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 816 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-030-607-14

Query Match      27.5%; Score 413.4; DB 3; Length 816;
Best Local Similarity 92.0%; Pred. No. 1.3e-100;
Matches 459; Conservative 0; Mismatches 37; Indels 3; Gaps 3;

QY 9 CACGAGCAGCAGACTCTGCAAGAGTTTCGTTATGAGAGGCTGCTGGGCAACAGCAAC 68
DB 498 CCNCGGAGCAGATNTGCAAGAGTTT-GTTTANGGGGNTGNTTGGGCAACAGCAAC 440
QY 69 TACC-TTCGGGAAGAGAGTGCAATTTAGCCTGTGCGGGGTGTGCAAGGT-GGGCCTTTGA 126
DB 439 TACCTTTCCGGAAGAGAGTTTCCATTCTAGCCTGTGCGGGGTGTGCAAGGTGGGCTTTGA 380
QY 127 GAGCAGCTCTGGGGCTCAGGCGACTTTTCCCGCAGGGGCCCTCCATGGAAGGGCGCATC 186
DB 379 GAGCAGTNTTGGGGNTCAGGAGCTTTTCCCNCAAGGGGCCNTNNCATGGAAGGGCGCATC 320
QY 187 CAGTGTGCTCTGGCACTGTGAGCCACCCAGTTTCCGCTGAGCAATGGCTGTGCAATCG 246
DB 319 CAGTGTGCTCTGGCACTGTGAGCCACCCAGTTTCCGCTGAGCAATGGCTGTGCAATNG 260
QY 247 ACAGTTTCTGGAGTGTGAGCAGACACCCCGCACTGCGCGCGGCTTCCGAGAGGCTGCCT 306
DB 259 ACAGTTTCTGGAGTGTGAGCAGACACCCCGCACTGCGCGCGGCTTCCGAGAGGCTGCCT 200
QY 307 GTGAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCGCCAGGACAAAG 366
DB 199 GTGAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCGCCAGTGAAGAAG 140
QY 367 GGCACTCGTGGAGCTCCGAGACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACT 426
DB 139 GGCACTCGTGGAGCTCCGAGACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACT 80
QY 427 ACAACCCCTTCAGCGACACTGGCGCGCTTACCTATGCTGTGTTAGCGCAACAAG 486
DB 79 ACAACCCCTTCAGCGACACTGGCGCGCTTACCTATGCTGTGTTAGCGCAACAAG 20
QY 487 ACACTTTTGAGGAGAGCA 505
DB 19 ACACTTTTGAGGAGAGCA 1

RESULT 6
US-09-439-313-14/c
; Sequence 14, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 816

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; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(816)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-14

Query Match      27.5%; Score 413.4; DB 4; Length 816;
Best Local Similarity 92.0%; Pred. No. 1.3e-100;
Matches 459; Conservative 0; Mismatches 37; Indels 3; Gaps 3;

QY 9 CACGAGCAGCAGACTCTGCAAGAGTTTCGTTATGAGAGGCTGCTGGGCAACAGCAAC 68
DB 498 CCNCGGAGCAGATNTGCAAGAGTTT-GTTTANGGGGNTGNTTGGGCAACAGCAAC 440
QY 69 TACC-TTCGGGAAGAGAGTGCAATTTAGCCTGTGCGGGGTGTGCAAGGT-GGGCCTTTGA 126
DB 439 TACCTTTCCGGAAGAGAGTTTCCATTCTAGCCTGTGCGGGGTGTGCAAGGTGGGCTTTGA 380
QY 127 GAGCAGCTCTGGGGCTCAGGCGACTTTTCCCGCAGGGGCCCTCCATGGAAGGGCGCATC 186
DB 379 GAGCAGTNTTGGGGNTCAGGAGCTTTTCCCNCAAGGGGCCNTNNCATGGAAGGGCGCATC 320
QY 187 CAGTGTGCTCTGGCACTGTGAGCCACCCAGTTTCCGCTGAGCAATGGCTGTGCAATCG 246
DB 319 CAGTGTGCTCTGGCACTGTGAGCCACCCAGTTTCCGCTGAGCAATGGCTGTGCAATNG 260
QY 247 ACAGTTTCTGGAGTGTGAGCAGACACCCCGCACTGCGCGCGGCTTCCGAGAGGCTGCCT 306
DB 259 ACAGTTTCTGGAGTGTGAGCAGACACCCCGCACTGCGCGCGGCTTCCGAGAGGCTGCCT 200
QY 307 GTGAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCGCCAGGACAAAG 366
DB 199 GTGAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCGCCAGTGAAGAAG 140
QY 367 GGCACTCGTGGAGCTCCGAGACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACT 426
DB 139 GGCACTCGTGGAGCTCCGAGACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACT 80
QY 427 ACAACCCCTTCAGCGACACTGGCGCGCTTACCTATGCTGTGTTAGCGCAACAAG 486
DB 79 ACAACCCCTTCAGCGACACTGGCGCGCTTACCTATGCTGTGTTAGCGCAACAAG 20
QY 487 ACACTTTTGAGGAGAGCA 505
DB 19 ACACTTTTGAGGAGAGCA 1

RESULT 7
US-09-352-616A-14/c
; Sequence 14, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqui
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427CB
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(816)

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OTHER INFORMATION: n = A,T,C or G  
US-09-352-616A-14

Query Match 27.5%; Score 413.4; DB 4; Length 816;  
Best Local Similarity 92.0%; Pred. No. 1.3e-100;  
Matches 459; Conservative 0; Mismatches 37; Indels 3; Gaps 3;

QY 9 CACGAGGAGCAGATCTCCAGAGTTTCGTTATGGAGGCTGCTTGGGCAACAGAACAC 68  
DB 498 CCNCGGAGCAGATNTGCAAGAGTTT-GTTTANGGGGNTGGNTTGGGCAACAGAACAC 440  
QY 69 TACC-TTCGGGGAAGAGTGCATTTAGCTGTGCGGGTGTGCAAGGT-GGGCCTTTGA 126  
DB 439 TACCTTTCCGGAAGAGATTCATTTAGCTGTGCGGGTGTGCAAGGTGGGGCCTTTGA 380  
QY 127 GAGGAGCTCTGGGGCTCAGGCGATTTCCGCCAGGGCCCTCCATGGAAAGGCGGCATC 186  
DB 379 GAGGAGCTNTGGGGNTCAGGAGTTTCCNCGAGGGCCNTNNCATGGAAAGGCGGCATC 320  
QY 187 CAGTGTCTCTGGCAGCTGTGAGCCACCCAGTTCGGCTGCGAGCAATGCTGTGATCG 246  
DB 319 CAGTGTCTCTGGCAGCTGTGAGCCACCCAGTTCGGCTGCGAGCAATGCTGTGATCG 260  
QY 247 ACAGTTTCTGGAGTGTGAGCAGACACCCCACTGCCCGCGCTCCGAGAGGCTGCCT 306  
DB 259 ACAGTTTCTGGAGTGTGAGCAGACACCCCACTGCCCGCGCTCCGAGAGGCTGCCT 200  
QY 307 GTGAAATACAGAGTGTGAGCAGACACCCCACTGCCCGCGCTCCGAGAGGCTGCCT 366  
DB 199 GTGAAATACAGAGTGTGAGCAGACACCCCACTGCCCGCGCTCCGAGAGGCTGCCT 140  
QY 367 GGCAGCTGCTGGAGCTGTGAGCAGACACCCCACTGCCCGCGCTCCGAGAGGCTGCCT 426  
DB 139 GGCAGCTGCTGGAGCTGTGAGCAGACACCCCACTGCCCGCGCTCCGAGAGGCTGCCT 80  
QY 427 ACAACCCCTTCAGGAGACACTGCGCCGCTTTACCTATGTTGTTTACGCAACAAGA 486  
DB 79 ACAACCCCTTCAGGAGACACTGCGCCGCTTTACCTATGTTGTTTACGCAACAAGA 20  
QY 487 ACAACTTTGAGGAAGAGCA 505  
DB 19 ACAACTTTGAGGAAGAGCA 1

RESULT 8  
US-09-232-149A-14/c  
Sequence 14, Application US/09232149A  
Patent No. 6465611  
GENERAL INFORMATION:

APPLICANT: Xu, Jianshun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer Lynn  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE  
FILE REFERENCE: 210121.427C6  
CURRENT APPLICATION NUMBER: US/09/232,149A  
CURRENT FILING DATE: 1999-01-15  
NUMBER OF SEQ ID NOS: 338  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 14  
LENGTH: 816  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(816)  
OTHER INFORMATION: n = A,T,C or G

Query Match 27.5%; Score 413.4; DB 4; Length 816;  
Best Local Similarity 92.0%; Pred. No. 1.3e-100;  
Matches 459; Conservative 0; Mismatches 37; Indels 3; Gaps 3;

QY 9 CACGAGGAGCAGATCTCCAGAGTTTCGTTATGGAGGCTGCTTGGGCAACAGAACAC 68  
DB 498 CCNCGGAGCAGATNTGCAAGAGTTT-GTTTANGGGGNTGGNTTGGGCAACAGAACAC 440  
QY 69 TACC-TTCGGGGAAGAGTGCATTTAGCTGTGCGGGTGTGCAAGGT-GGGCCTTTGA 126  
DB 439 TACCTTTCCGGAAGAGATTCATTTAGCTGTGCGGGTGTGCAAGGTGGGGCCTTTGA 380

QY 9 CACGAGGAGCAGATCTCCAGAGTTTCGTTATGGAGGCTGCTTGGGCAACAGAACAC 68  
DB 498 CCNCGGAGCAGATNTGCAAGAGTTT-GTTTANGGGGNTGGNTTGGGCAACAGAACAC 440  
QY 69 TACC-TTCGGGGAAGAGTGCATTTAGCTGTGCGGGTGTGCAAGGT-GGGCCTTTGA 126  
DB 439 TACCTTTCCGGAAGAGATTCATTTAGCTGTGCGGGTGTGCAAGGTGGGGCCTTTGA 380  
QY 127 GAGGAGCTCTGGGGCTCAGGCGATTTCCGCCAGGGCCCTCCATGGAAAGGCGGCATC 186  
DB 379 GAGGAGCTNTGGGGNTCAGGAGTTTCCNCGAGGGCCNTNNCATGGAAAGGCGGCATC 320  
QY 187 CAGTGTCTCTGGCAGCTGTGAGCCACCCAGTTCGGCTGCGAGCAATGCTGTGATCG 246  
DB 319 CAGTGTCTCTGGCAGCTGTGAGCCACCCAGTTCGGCTGCGAGCAATGCTGTGATCG 260  
QY 247 ACAGTTTCTGGAGTGTGAGCAGACACCCCACTGCCCGCGCTCCGAGAGGCTGCCT 306  
DB 259 ACAGTTTCTGGAGTGTGAGCAGACACCCCACTGCCCGCGCTCCGAGAGGCTGCCT 200  
QY 307 GTGAAATACAGAGTGTGAGCAGACACCCCACTGCCCGCGCTCCGAGAGGCTGCCT 366  
DB 199 GTGAAATACAGAGTGTGAGCAGACACCCCACTGCCCGCGCTCCGAGAGGCTGCCT 140  
QY 367 GGCAGCTGCTGGAGCTGTGAGCAGACACCCCACTGCCCGCGCTCCGAGAGGCTGCCT 426  
DB 139 GGCAGCTGCTGGAGCTGTGAGCAGACACCCCACTGCCCGCGCTCCGAGAGGCTGCCT 80  
QY 427 ACAACCCCTTCAGGAGACACTGCGCCGCTTTACCTATGTTGTTTACGCAACAAGA 486  
DB 79 ACAACCCCTTCAGGAGACACTGCGCCGCTTTACCTATGTTGTTTACGCAACAAGA 20  
QY 487 ACAACTTTGAGGAAGAGCA 505  
DB 19 ACAACTTTGAGGAAGAGCA 1

RESULT 9  
US-09-159-812-14/c  
Sequence 14, Application US/09159812A  
Patent No. 6613872  
GENERAL INFORMATION:

APPLICANT: Xu, Jianshun  
APPLICANT: Dillon, Davin C.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF  
FILE REFERENCE: 210121.428C5  
CURRENT APPLICATION NUMBER: US/09/159,812A  
CURRENT FILING DATE: 1998-09-23  
NUMBER OF SEQ ID NOS: 306  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 14  
LENGTH: 816  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(816)  
OTHER INFORMATION: n = A,T,C or G

Query Match 27.5%; Score 413.4; DB 4; Length 816;  
Best Local Similarity 92.0%; Pred. No. 1.3e-100;  
Matches 459; Conservative 0; Mismatches 37; Indels 3; Gaps 3;

QY 9 CACGAGGAGCAGATCTCCAGAGTTTCGTTATGGAGGCTGCTTGGGCAACAGAACAC 68  
DB 498 CCNCGGAGCAGATNTGCAAGAGTTT-GTTTANGGGGNTGGNTTGGGCAACAGAACAC 440  
QY 69 TACC-TTCGGGGAAGAGTGCATTTAGCTGTGCGGGTGTGCAAGGT-GGGCCTTTGA 126  
DB 439 TACCTTTCCGGAAGAGATTCATTTAGCTGTGCGGGTGTGCAAGGTGGGGCCTTTGA 380

127 GAGGAGAGCTCTGGGGCTCAGGCGACTTTCCCGCCAGGCCCCCTTCCATGGAAAGGCGCCATC 186  
 379 GAGGAGAGTNTGGGNTCAGGAGCTTTCCCGCCAGGCCCCCTTCCATGGAAAGGCGCCATC 320  
 187 CAGTGTCTCTGGGCTCAGGCGACTTTCCCGCCAGGCCCCCTTCCATGGAAAGGCGCCATC 246  
 319 CAGTGTCTCTGGGCTCAGGCGACTTTCCCGCCAGGCCCCCTTCCATGGAAAGGCGCCATC 260  
 247 ACAGTTTCTGGAGTGTGACGACACACCCCACTGCGCCCGAGCGCTCCGACGAGGCTGCT 306  
 259 ACAGTTTCTGGAGTGTGACGACACACCCCACTGCGCCCGAGCGCTCCGACGAGGCTGCT 200  
 307 GTGAAAATACAGAGTGTGACGACACACCCCACTGCGCCCGAGCGCTCCGACGAGGCTGCT 366  
 199 GTGAAAATACAGAGTGTGACGACACACCCCACTGCGCCCGAGCGCTCCGACGAGGCTGCT 140  
 367 GGCACCTGCGTGGACCTGCGACACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGCTACT 426  
 139 GGCACCTGCGTGGACCTGCGACACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGCTACT 80  
 427 ACAACCCCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 486  
 79 ACAACCCCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 20  
 487 ACAACTTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 505  
 19 ACAACTTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1

RESULT 10  
 US-09-636-215-14/c  
 ; Sequence 14, Application US/09636215  
 ; Patent No. 6620922  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillon, Davin C.  
 ; APPLICANT: Mitcham, Jennifer L.  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Jiang, Yuqi  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Day, Craig H.  
 ; APPLICANT: Vedvick, Thomas S.  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Li, Samuel  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Hepler, William  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; FILE REFERENCE: 210121.4217C17  
 ; CURRENT APPLICATION NUMBER: US/09/636,215  
 ; CURRENT FILING DATE: 2000-08-10  
 ; NUMBER OF SEQ ID NOS: 852  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 14  
 ; LENGTH: 816  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(816)  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-09-636-215-14

Query Match 27.5%; Score 413.4; DB 4; Length 816;  
 Best Local Similarity 92.0%; Pred. No. 1.3e-100;  
 Matches 459; Conservative 0; Mismatches 37; Indels 3; Gaps 3;  
 9 CACGAGGAGCAGATCTCGAAGAGTTTCGTTATGAGGCTGCTTGGGCAACAGAGCAAC 68

498 CCNCGGAGCAGATCTGCAAGAGTTTGTTCAGGGGNTGNTTGGCAACAGAGAAAC 440  
 69 TACC-TTCGGGAGAGAGAGTGCATTTCTAGCTGTCTGGGGTGTGCAAGT-GGGCTTTGA 126  
 439 TACCTTTGGGAGAGAGATTCATTTCTAGCTGTCTGGGGTGTGCAAGTGGGGCTTTGA 380  
 127 GAGCAGCTCTGGGGCTCAGGCGACTTTCCCGCCAGGCCCCCTTCCATGGAAAGGCGCCATC 186  
 379 GAGGAGAGTNTGGGNTCAGGAGCTTTCCCGCCAGGCCCCCTTCCATGGAAAGGCGCCATC 320  
 187 CAGTGTCTCTGGGCTCAGGCGACTTTCCCGCCAGGCCCCCTTCCATGGAAAGGCGCCATC 246  
 319 CAGTGTCTCTGGGCTCAGGCGACTTTCCCGCCAGGCCCCCTTCCATGGAAAGGCGCCATC 260  
 247 ACAGTTTCTGGAGTGTGACGACACACCCCACTGCGCCCGAGCGCTCCGACGAGGCTGCT 306  
 259 ACAGTTTCTGGAGTGTGACGACACACCCCACTGCGCCCGAGCGCTCCGACGAGGCTGCT 200  
 307 GTGAAAATACAGAGTGTGACGACACACCCCACTGCGCCCGAGCGCTCCGACGAGGCTGCT 366  
 139 GTGAAAATACAGAGTGTGACGACACACCCCACTGCGCCCGAGCGCTCCGACGAGGCTGCT 140  
 367 GGCACCTGCGTGGACCTGCGACACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGCTACT 426  
 139 GGCACCTGCGTGGACCTGCGACACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGCTACT 80  
 427 ACAACCCCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 486  
 79 ACAACCCCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 20  
 487 ACAACTTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 505  
 19 ACAACTTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1

RESULT 11  
 US-09-685-166A-14/c  
 ; Sequence 14, Application US/09685166A  
 ; Patent No. 6630305  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillon, Davin C.  
 ; APPLICANT: Mitcham, Jennifer L.  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Jiang, Yuqi  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Day, Craig H.  
 ; APPLICANT: Vedvick, Thomas S.  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Li, Samuel  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Hepler, William  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; FILE REFERENCE: 210121.427C21  
 ; CURRENT APPLICATION NUMBER: US/09/685,166A  
 ; CURRENT FILING DATE: 2000-10-10  
 ; NUMBER OF SEQ ID NOS: 898  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 14  
 ; LENGTH: 816  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(816)  
 ; OTHER INFORMATION: n = A,T,C or G

US-09-685-166A-14

Query Match 27.5%; Score 413.4; DB 4; Length 816;  
Best Local Similarity 92.0%; Pred. No. 1.3e-100;  
Matches 459; Conservative 0; Mismatches 37; Indels 3;  
Gaps 3;

9	QY	CACGAGGACGAGTCTGCAAGAGTTTCGTTTATGAGGCTGCTTGGCCACACGAACAAC	68
498	DB	CCNCGCGAGCAGATNTGCAAGAGTTT-GTTTANGGGGNTGGNTTGGGCAACAAGAAAC	440
69	QY	TACC-TTGGGAGAAGAGTGCAATCTAGCCTGTGCGGGGTGTGCAAGGT-GGGCCTTTGA	126
439	DB	TACCTTTCGGGAAGAGATTCCATTCTAGCCTGTGCGGGGTGCAAGGTGGGCTTTGA	380
127	QY	GAGCGAGCTCTGGGCTCAGCGAGCTTTCGCCAGAGGCCCTCCATGGAAGAGGCCCATC	186
379	DB	GAGCGAGNTTGGGNTCAGGAGCTTTCCNCAGGGCCNTNNCATGGAAGAGGCCCATC	320
187	QY	CAGTGTGCTCTGGCACCTGTGAGGCCACCCAGATTCCGCTGCAGCAATGGCTGTGTCATG	246
319	DB	CAGTGTGCTCTGGCAGTCAGGCCACCCAGATTCCGCTGCAGCAATGGCTGTGTCATG	260
247	QY	ACAGTTTCTGGAGTGTGACGACACCCCAACTGCCCCGAGCGCTCCGACGAGCTGCCT	306
259	DB	ACAGTTTCTGGAGTGTGAAACACCCCAACTGCCCCGAGCGCTCCGACGAGCTGCCT	200
307	QY	GTGAAAAATACACGAGTGGCTTTTCAGCAGCTCCAGCGCATCCATTCCCGACGACAAAG	366
199	DB	GTGAAAAATACAGAGTGGCTTTTCAGCAGCTCCAGCGCATCCATTCCCGAGTGCAAAG	140
367	QY	GGCACTGGTGGAACTTGCACAGACACAGGACTCTCGAAGGAGAGCATCCCGGCTGTGACT	426
139	DB	GGCACTGGTGGAACTTGCACAGACACAGGACTCTCGAAGGAGAGCATCCCGGCTGTGACT	80
427	QY	ACAACCCCTTCAGGGAACACTGCGCCCGCTTTACTATGTGGTGTGTATCGCCAAACAAG	486
79	DB	ACAACCCCTTCAGGGAACACTGCGCCCGCTTTACTATGTGGTGTGTATCGCCAAACAAG	20
487	QY	ACAACCTTGGAGGAGACA	505
19	DB	ACAACCTTGGAGGAGCA	1

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RESULT 12
US-09-115-453-14/c
; Sequence 14, Application US/09115453B
; Patent No. 6657056
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(816)
; OTHER INFORMATION: n = A,T,C or G
US-09-115-453-14

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Query Match	27.5%	Score 413.4;	DB 4;	Length 816;
Best Local Similarity	92.0%;	Pred. No. 1.3e-100;		
Matches 459;	Conservative	0;	Mismatches 37;	Indels 3;
Gaps				3
Qy	9	CACGAGGACGAGATCTGCAAGAGTTTCGTTTATGGAGCGCTGCTCGGCGACAGAGAACAC		68

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498 CCNCGGAGCAGATNTGCAAGAGTTT-GTTTANGGGGNTGGNTTGGCCACCAAGAANAAC 444
69 TACC-TTGGGGAAGAGAGTGCAATTTAGCCTGTCCGGGTGTGCAAGGT-GGGCCTTTGA 126
439 TACCTTTTGGGGAAGAGATTCCAATTTAGCCTGTCCGGGTGTGCAAGGTGGGGCNTTTTGA 380
127 GAGCGAGCTCTGGGGCTTCAGGCGACTTTCCCCAGGGCCCCCTCCATGTGAAAGGCGCCATC 186
379 GAGCGAGNTGTGGGNTCAGGAGCTTTCCNCAGGGCCCNNTNNCATGGAAGAGCGCCATC 320
187 CAGTGTGCTTGGGCACTGTTCAGCCCAACCCAGTTTCGGCTGCGAGCATAGCTCTGCATCG 246
319 CAGTGTGCTTGGGCACTGTTCAGCCCAACCCAGTTTCGGCTGCGAGCAATAGCTCTGCTGNTG 260
247 ACAGTTTCTTGGAGTGTGACGACACCCCAACTGCCCGCAGCGCTCCGACGAGGCTGCT 306
259 ACAGTTTCTTGGAGTGTGGAAGACACCCCAACTGCCCGCAGCGCTCCGACGAGGCTGCT 200
307 GTGAAATAATACACAGTGGCTTTGACGAGCTCCAGCGCATCCCAATTTCCCGACGACAAAG 366
199 GTGAAATAATACACAGTGGCTTTGACGAGCTCCAGCGCATCCCAATTTCCCGACGACAAAG 140
367 GGCAGTGGCTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACT 426
139 GGCAGTGGCTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACT 80
427 ACAACCCCTTCAGCGACACTGGCCCGCTTTACCTATGTGTGTTTACGGCAACAAGA 486
79 ACAACCCCTTCAGCGACACTGGCCCGCTTTACCTATGTGTGTTTATGGCNACAAGA 20
487 ACAACTTTGAGGAAGACGA 505
19 ACAACTTTGAGGAAGACGA 1

RESULT 13
US-09-688-489-14/c
; Sequence 14, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun H.
; APPLICANT: Dillon, Jennifer Lynn
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(816)
; OTHER INFORMATION: n = A,T,C or G
; US-09-688-489-14

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	Query Match	27.5%	Score 413.4	DB 4	Length 816
	Best Local Similarity	92.0%	Pred. No. 1.3e-100		
	Matches 459	Conservative	0	Mismatches 37	Indels 3
Qy	9	CACGAGGACGATCTGCAAGAGTTTCGTTTATGGAGGCTCTGGGCAACAAGAACAC	68		
Db	498	CCNCGGAGCAGATNTCCAGAGTTT-GTTTANGGGTGGTGGTGGCAACAGARNAC	440		
Qy	69	TACC-TTTCGGGACAGAGTGCAATTCCTAGCCTGTTCGGGGTGTGCAAGT-GGGCCTTTGA	126		
Db	439	TACCTTTCGGGACAGAGTTCCATTCCTAGCCTGTTCGGGGTGTGCAAGTGGGGCCTTTGA	380		
Qy	127	GAGGCACTCTGGGGCTCAGCGGCACTTTCCCCCAAGGGCCCCCTCATGGAAAGGGCCCATC	186		

Db 379 GAGCGAGTNTGGGNTCAGGAGCTTTCCNCAGAGGCCCTNNNCATGGAAAGCGGCATC 320  
Qy 187 CAGTGTCTCTGACACTGTACGCCACCCAGTTCCTGCTGCAGCAATGGTGTGTCATCG 246  
Db 319 CAGTGTCTCTGACANTGTACGCCACCCAGTTCCTGCTGCAGCAATGGTGTGTCATNG 260  
Qy 247 ACAGTTTCTGAGTGTGACGACACCCCACTGCCCCGAGCGCTCCGACGAGGCTGCCT 306  
Db 259 ACAGTTTCTGAGTGTGAGACACACCCCACTGCCCCGAGCGGTCCGACGAGGCTGCCT 200  
Qy 307 GTCAAAATAACAGAGTGGCTTTGAGAGCTCCAGGCGCATCCATTTCCCGAGGACAAAG 366  
Db 199 GTCAAAATAACAGAGTGGCTTTGAGAGCTCCAGGCGCATCCATTTCCCGAGTGAAGAAG 140  
Qy 367 GGCACTGCTGAGCTGCGCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGTACT 426  
Db 139 GGCACTGCTGAGCTGCGCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGTACT 80  
Qy 427 ACAACCCCTTCAGCGAACTGCGCGCGCTTTACTTACCTATGTTGTTAGCGGCAAGA 486  
Db 79 ACAACCCCTTCAGCGAACTGCGCGCGCTTTACTTACCTATGTTGTTAGCGGCAAGA 20  
Qy 487 ACAACTTTGAGGAAGACGA 505  
Db 19 ACACTTTGAGGAAGACGA 1

RESULT 14  
US-09-935-390a-4.rni  
; Sequence 37, Application US/09020956  
; Patent No. 6261562  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillin, David C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
; NUMBER OF SEQUENCES: 178  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; APPLICATION NUMBER: US/09/020,956  
; FILING DATE: 09-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.427C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 760 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-09-935-390a-4.rni

Query Match 23.88; Score 357.8; DB 3; Length 760;  
Best Local Similarity 90.28; Pred. No. 8.4e-86;  
Matches 432; Conservative 0; Mismatches 39; Indels 8; Gaps 5;

Qy 32 TTTCGTTTATGAGGCTGCTTGGGCAACAGAACTACCTTCGGGAGAGAGTGCA - 90  
Db 476 TTGGTTTGTGAGGCTGCTTGGGCAACAGAACTACCTTCGGGAGAGAGTGCA 417  
Qy 91 TTCTAGCTGCTGAGGCTGCTTGGGCAACAGAACTACCTTCGGGAGAGAGTGCA 150  
Db 416 TTCTAGCTGCTGAGGCTGCTTGGGCAACAGAACTACCTTCGGGAGAGAGTGCA 362  
Qy 151 TTTCGTTTATGAGGCTGCTTGGGCAACAGAACTACCTTCGGGAGAGAGTGCA 210  
Db 361 GATTTTCCCGGAGGCTGCTTGGGCAACAGAACTACCTTCGGGAGAGAGTGCA 303  
Qy 211 CCACCCAGTTCGCTGAGGCTGCTTGGGCAACAGAACTACCTTCGGGAGAGAGTGCA 269  
Db 302 CCACCCAGTTCGCTGAGGCTGCTTGGGCAACAGAACTACCTTCGGGAGAGAGTGCA 243  
Qy 270 ACCCCCACTGCTGAGGCTGCTTGGGCAACAGAACTACCTTCGGGAGAGAGTGCA 329  
Db 242 ACCCCCACTGCTGAGGCTGCTTGGGCAACAGAACTACCTTCGGGAGAGAGTGCA 183  
Qy 330 GACGAGCTTCAGGCTGCTTGGGCAACAGAACTACCTTCGGGAGAGAGTGCA 389  
Db 182 GACGAGCTTCAGGCTGCTTGGGCAACAGAACTACCTTCGGGAGAGAGTGCA 123  
Qy 390 ACAGGACTCTGCAAGGAGAGCATCCCGGCTGCTTGGGCAACAGAACTACCTTCGGGAGAGAGTGCA 449  
Db 122 ACAGGACTCTGCAAGGAGAGCATCCCGGCTGCTTGGGCAACAGAACTACCTTCGGGAGAGAGTGCA 63  
Qy 450 GCGCGTTTACCTATGCTGCTTGGGCAACAGAACTACCTTCGGGAGAGAGTGCA 508  
Db 62 GCGCGTTTACCTATGCTGCTTGGGCAACAGAACTACCTTCGGGAGAGAGTGCA 4

RESULT 15  
US-09-935-390a-4.rni  
; Sequence 37, Application US/09030607  
; Patent No. 6262245  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillin, David C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FC  
; NUMBER OF SEQUENCES: 224  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; APPLICATION NUMBER: US/09/030,607  
; FILING DATE: 25-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.427C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 760 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-09-935-390a-4.rni

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Query Match      23.8%; Score 357.8; DB 3; Length 760;
Best Local Similarity 90.2%; Pred. No. 8.4e-86;
Matches 432; Conservative 0; Mismatches 39; Indels 8; Gaps 5;

Qy 32 TTTGTTTATGAGGCTGCTTGGGCAACAAGAACAACTACCTTCGGGAAGAGTGCAC- 90
Db 476 TTTGTTTATGAGGCTGCTTGGGCAACAAGAACAACTACCTTCGGGAAGAGTGCAT 417

Qy 91 TTTAGCCTGTGCGGGTGTGCAAGTGGGCTTTGAGAGGAGCTCTGGGGCTCAGGCA 150
Db 416 TTTAGCCTGTGCGGGTGTGCAAGT-GGCTTTGAGAGGAGCTTTGGG-----NTNAGN 362

Qy 151 CTTTCCCCCAGGGCCCCCTCCATGGAAGGGCCCATCCAGTGTCTGTGGCACTGTGAGC 210
Db 361 GATTTCCCCCAGGGCCCCCTCCATGGAAGGGC-CNATCCAGTGTCTGTGGCACCTGTGAGC 303

Qy 211 CCAGCCAGTTCGGCTGCGAGCAAT-GGCTGTGCAATCGACAGTTTCCTGGAGTGTGAGC 269
Db 302 CCAGCCAGTTCGGCTGCGAGCAATGGGCTGNTGNATCGACAGTTTAGTGGAGTGTGAGC 243

Qy 270 ACCCCCAACTGCCCGAGCGCCTCCGACCGAGGCTGCTGTGAAAAATACAGAGTGGCTTT 329
Db 242 ACCCCCAACTGCCCGAGCGCTTCGGAGGAGGCTGCTGTGAAAAATACAGAGTGGNTTN 183

Qy 330 GACGAGCTCCAGCGCATCCATTTCCCGAGCGACAAAGGGCACTGCGTGGACCTGCCAGAC 389
Db 182 GACGAGCTCCAGCGCATCCATTTCCCGAGTGCACAAAGGGCAATTCGTGGACCTGCCAGAC 123

Qy 390 ACAGGACTCTGCAAGGAGAGCATCCGGCGCTGGTACTACAAACCCCTTCAGCGAACACTGC 449
Db 122 ACAGGACTCTGCAAGGAGAGCATCCGGCGCTGGTACTACAAACCCCTTCAGCGAACACTGC 63

Qy 450 GCGCGCTTTACTATGGTGGTGTGTAACGCGCAACAAGAACAACTTTGAGGAAGAGAGCA 508
Db 62 GCGCGCTTTACTATGGTGGTGTGTAACGCGCAACAAGAACAACTTTGAGGAAGAGAGCA 4

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Search completed: April 22, 2004, 08:12:04  
Job time : 125 secs



Qy 1 MERRHPVCSGTCTQPTQRCNSGCCIDSFLECDTPNCPDASDEAAACEKYSFGDELQRIH 60  
Db 143 MERRHPVCSGTCTQPTQRCNSGCCIDSFLECDTPNCPDASDEAAACEKYSFGDELQRIH 202  
Qy 61 FPSDKGHCVLDPTGLCKESIPRWYNPFSEHCARFTYGGCYGNKNFEEQOCLSCRG 120  
Db 203 FPSDKGHCVLDPTGLCKESIPRWYNPFSEHCARFTYGGCYGNKNFEEQOCLSCRG 262  
Qy 121 ISKDVFGRLREIPIPTSGVEMAVAVFLVICIVVVAIIIGCYFFKQKQKDFGHHHPP 180  
Db 263 ISKDVFGRLREIPIPTSGVEMAVAVFLVICIVVVAIIIGCYFFKQKQKDFGHHHPP 322  
Qy 181 PTPASSTVSTTTEDTEHLVYNHTTRPL 206  
Db 323 PTPASSTVSTTTEDTEHLVYNHTTRPL 348

## RESULT 2

US-08-685-558A-18  
; Sequence 18, Application US/08685558A  
; Patent No. 6225081  
; GENERAL INFORMATION:  
; APPLICANT: SHIMOMURA, Takeshi  
; APPLICANT: KAWAGUCHI, Toshiya  
; APPLICANT: KITAMURA, Naomi  
; APPLICANT: MIYAZAWA, Keiji  
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME  
; TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,558A  
FILING DATE: 24-JUL-1996  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NUMBER: JPA Hei 7-187135  
FILING DATE: 24-JUL-1995  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 513 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: MKN45

US-08-685-558A-18

Query Match 100.0%; Score 206; DB 3; Length 513;  
Best Local Similarity 100.0%; Pred. No. 1.5e-187;  
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MERRHPVCSGTCTQPTQRCNSGCCIDSFLECDTPNCPDASDEAAACEKYSFGDELQRIH 60  
Db 308 MERRHPVCSGTCTQPTQRCNSGCCIDSFLECDTPNCPDASDEAAACEKYSFGDELQRIH 367  
Qy 61 FPSDKGHCVLDPTGLCKESIPRWYNPFSEHCARFTYGGCYGNKNFEEQOCLSCRG 120  
Db 368 FPSDKGHCVLDPTGLCKESIPRWYNPFSEHCARFTYGGCYGNKNFEEQOCLSCRG 427  
Qy 121 ISKDVFGRLREIPIPTSGVEMAVAVFLVICIVVVAIIIGCYFFKQKQKDFGHHHPP 180

Db 428 ISKDVFGRLREIPIPTSGVEMAVAVFLVICIVVVAIIIGCYFFKQKQKDFGHHHPP 487  
Qy 181 PTPASSTVSTTTEDTEHLVYNHTTRPL 206  
Db 488 PTPASSTVSTTTEDTEHLVYNHTTRPL 513

## RESULT 3

US-09-765-449-18  
; Sequence 18, Application US/09765449  
; Patent No. 6465622  
; GENERAL INFORMATION:  
; APPLICANT: SHIMOMURA, Takeshi  
; APPLICANT: KAWAGUCHI, Toshiya  
; APPLICANT: KITAMURA, Naomi  
; APPLICANT: MIYAZAWA, Keiji  
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME  
; TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,449  
FILING DATE: 22-Jan-2001  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NUMBER: 08/685,558  
FILING DATE: <Unknown>  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 513 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: MKN45  
; SEQUENCE DESCRIPTION: SEQ ID NO: 18  
; US-09-765-449-18

Query Match 100.0%; Score 206; DB 4; Length 513;  
Best Local Similarity 100.0%; Pred. No. 1.5e-187;  
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MERRHPVCSGTCTQPTQRCNSGCCIDSFLECDTPNCPDASDEAAACEKYSFGDELQRIH 60  
Db 308 MERRHPVCSGTCTQPTQRCNSGCCIDSFLECDTPNCPDASDEAAACEKYSFGDELQRIH 367  
Qy 61 FPSDKGHCVLDPTGLCKESIPRWYNPFSEHCARFTYGGCYGNKNFEEQOCLSCRG 120  
Db 368 FPSDKGHCVLDPTGLCKESIPRWYNPFSEHCARFTYGGCYGNKNFEEQOCLSCRG 427  
Qy 121 ISKDVFGRLREIPIPTSGVEMAVAVFLVICIVVVAIIIGCYFFKQKQKDFGHHHPP 180  
Db 428 ISKDVFGRLREIPIPTSGVEMAVAVFLVICIVVVAIIIGCYFFKQKQKDFGHHHPP 487  
Qy 181 PTPASSTVSTTTEDTEHLVYNHTTRPL 206  
Db 488 PTPASSTVSTTTEDTEHLVYNHTTRPL 513

## RESULT 4

```
US-09-312-283C-182
; Sequence 182, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; FILE REFERENCE: 11000.101122
; CURRENT APPLICATION NUMBER: US/09/312,283C
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Mouse
;
US-09-312-283C-182

Query Match      13.1%; Score 27; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 2.6e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 HHPPTPASSTVSTTDTTEHLVYNHTT 203
DB 43 HHPPTPASSTVSTTDTTEHLVYNHTT 69

RESULT 5
US-09-188-930-182
; Sequence 182, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.101121
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 182
; LENGTH: 72
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: {64}...{64}
US-09-188-930-182

Query Match      10.2%; Score 21; DB 3; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 HHPPTPASSTVSTTDTTEHL 197
DB 43 HHPPTPASSTVSTTDTTEHL 63

RESULT 6
5208144-20
; Patent No. 5208144
; APPLICANT: SMITH, JOHN A.; RAYCHOWDHURY, RAKTIMA; NILES, JOHN L.
; TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN DNA
; CONTAINING THE GENE ENCODING LOW DENSITY LIPOPROTEIN RECEPTOR
;
US-09-040-774-2
; Sequence 2, Application US/09040774
; Patent No. 6207811
; GENERAL INFORMATION:
; APPLICANT: Trygsvason, Karl
; APPLICANT: Kestila, Marjo
; APPLICANT: Lenkkeri, Ulla
; APPLICANT: Mannikko, Minna
; TITLE OF INVENTION: Nephric Gene and Protein
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive, Suite 3200
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

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US-09-040-774-2
; Sequence 2, Application US/09040774
; Patent No. 6207811
; GENERAL INFORMATION:
; APPLICANT: Trygsvason, Karl
; APPLICANT: Kestila, Marjo
; APPLICANT: Lenkkeri, Ulla
; APPLICANT: Mannikko, Minna
; TITLE OF INVENTION: Nephric Gene and Protein
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive, Suite 3200
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

```
US-09-040-774-2
; Sequence 2, Application US/09040774
; Patent No. 6207811
; GENERAL INFORMATION:
; APPLICANT: Trygsvason, Karl
; APPLICANT: Kestila, Marjo
; APPLICANT: Lenkkeri, Ulla
; APPLICANT: Mannikko, Minna
; TITLE OF INVENTION: Nephric Gene and Protein
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive, Suite 3200
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

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US-09-040-774-2
; Sequence 2, Application US/09040774
; Patent No. 6207811
; GENERAL INFORMATION:
; APPLICANT: Trygsvason, Karl
; APPLICANT: Kestila, Marjo
; APPLICANT: Lenkkeri, Ulla
; APPLICANT: Mannikko, Minna
; TITLE OF INVENTION: Nephric Gene and Protein
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive, Suite 3200
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

```
US-09-040-774-2
; Sequence 2, Application US/09040774
; Patent No. 6207811
; GENERAL INFORMATION:
; APPLICANT: Trygsvason, Karl
; APPLICANT: Kestila, Marjo
; APPLICANT: Lenkkeri, Ulla
; APPLICANT: Mannikko, Minna
; TITLE OF INVENTION: Nephric Gene and Protein
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive, Suite 3200
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```



;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/040,774  
;; FILING DATE: 18 MAR 1998  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Chao, Mark  
;; REGISTRATION NUMBER: 37,293  
;; REFERENCE/DOCKET NUMBER: 97,842  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (312)913-0001  
;; TELEFAX: (312)913-0002  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1241 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-09-040-774-2

Query Match 3.9%; Score 8; DB 3; Length 1241;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 185 SSTVSTTE 192  
Db 1127 SSTVSTTE 1134

;; RESULT 9  
;; US-08-566-800A-32  
;; Sequence 32, Application US/08566800A  
;; Patent No. 5736364  
;; GENERAL INFORMATION:  
;; APPLICANT: Kelley, Robert F.  
;; APPLICANT: Lazarus, Robert A.  
;; APPLICANT: Lee, Geoffrey F.  
;; TITLE OF INVENTION: No. 5736364e1 Factor VIIa Inhibitors  
;; NUMBER OF SEQUENCES: 58  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Genentech, Inc.  
;; STREET: 460 Point San Bruno Blvd  
;; CITY: South San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94080  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: WinPatIn (Genentech)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/566,800A  
;; FILING DATE: 04-Dec-1995  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Kubinec, Jeffrey S.  
;; REGISTRATION NUMBER: 36,575  
;; REFERENCE/DOCKET NUMBER: P0958B  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415/225-8228  
;; TELEFAX: 415/952-9881  
;; TELEX: 910/371-7168  
;; INFORMATION FOR SEQ ID NO: 32:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 58 amino acids  
;; TYPE: Amino Acid  
;; TOPOLOGY: Linear

US-08-566-800A-32  
Query Match 3.4%; Score 7; DB 1; Length 58;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 185 SSTVSTTE 192  
Db 1127 SSTVSTTE 1134

QY 98 YGCGYCN 104  
Db 35 YGCGYCN 41  
;; RESULT 10  
;; US-08-566-800A-37  
;; Sequence 37, Application US/08566800A  
;; Patent No. 5736364  
;; GENERAL INFORMATION:  
;; APPLICANT: Kelley, Robert F.  
;; APPLICANT: Lazarus, Robert A.  
;; APPLICANT: Lee, Geoffrey F.  
;; TITLE OF INVENTION: No. 5736364e1 Factor VIIa Inhibitors  
;; NUMBER OF SEQUENCES: 58  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Genentech, Inc.  
;; STREET: 460 Point San Bruno Blvd  
;; CITY: South San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94080  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: WinPatIn (Genentech)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/566,800A  
;; FILING DATE: 04-Dec-1995  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Kubinec, Jeffrey S.  
;; REGISTRATION NUMBER: 36,575  
;; REFERENCE/DOCKET NUMBER: P0958B  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415/225-8228  
;; TELEFAX: 415/952-9881  
;; TELEX: 910/371-7168  
;; INFORMATION FOR SEQ ID NO: 37:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 58 amino acids  
;; TYPE: Amino Acid  
;; TOPOLOGY: Linear  
US-08-566-800A-37

Query Match 3.4%; Score 7; DB 1; Length 58;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 YGCGYCN 104  
Db 35 YGCGYCN 41

;; RESULT 11  
;; US-08-566-800A-38  
;; Sequence 38, Application US/08566800A  
;; Patent No. 5736364  
;; GENERAL INFORMATION:  
;; APPLICANT: Kelley, Robert F.  
;; APPLICANT: Lazarus, Robert A.  
;; APPLICANT: Lee, Geoffrey F.  
;; TITLE OF INVENTION: No. 5736364e1 Factor VIIa Inhibitors  
;; NUMBER OF SEQUENCES: 58  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Genentech, Inc.  
;; STREET: 460 Point San Bruno Blvd  
;; CITY: South San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94080  
;; COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/566,800A  
FILING DATE: 04-Dec-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kubinec, Jeffrey S.  
REGISTRATION NUMBER: 36,575  
REFERENCE/DOCKET NUMBER: P0958B  
TELEPHONE: 415/225-8228  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 58 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-566-800A-38

Query Match 3.4%; Score 7; DB 1; Length 58;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 98 YGCGYGN 104  
Db 35 YGCGYGN 41

RESULT 12  
US-08-566-800A-39  
Sequence 39, Application US/08566800A  
Patent No. 5736364  
GENERAL INFORMATION:  
APPLICANT: Kelley, Robert F.  
APPLICANT: Lazarus, Robert A.  
APPLICANT: Lee, Geoffrey F.  
TITLE OF INVENTION: No. 5736364el Factor VIIa Inhibitors  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/566,800A  
FILING DATE: 04-Dec-1995  
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: Kubinec, Jeffrey S.  
REGISTRATION NUMBER: 36,575  
REFERENCE/DOCKET NUMBER: P0958B  
TELEPHONE: 415/225-8228  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 58 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-566-800A-39

Query Match 3.4%; Score 7; DB 1; Length 58;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 98 YGCGYGN 104  
Db 35 YGCGYGN 41

RESULT 13  
US-08-566-800A-42  
Sequence 42, Application US/08566800A  
Patent No. 5736364  
GENERAL INFORMATION:  
APPLICANT: Kelley, Robert F.  
APPLICANT: Lazarus, Robert A.  
APPLICANT: Lee, Geoffrey F.  
TITLE OF INVENTION: No. 5736364el Factor VIIa Inhibitors  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/566,800A  
FILING DATE: 04-Dec-1995  
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: Kubinec, Jeffrey S.  
REGISTRATION NUMBER: 36,575  
REFERENCE/DOCKET NUMBER: P0958B  
TELEPHONE: 415/225-8228  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 58 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-566-800A-42

Query Match 3.4%; Score 7; DB 1; Length 58;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 98 YGCGYGN 104  
Db 35 YGCGYGN 41

RESULT 14  
US-08-566-800A-44  
Sequence 44, Application US/08566800A  
Patent No. 5736364  
GENERAL INFORMATION:  
APPLICANT: Kelley, Robert F.  
APPLICANT: Lazarus, Robert A.  
APPLICANT: Lee, Geoffrey F.  
TITLE OF INVENTION: No. 5736364el Factor VIIa Inhibitors  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco

STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/566,800A  
FILING DATE: 04-Dec-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kubinec, Jeffrey S.  
REGISTRATION NUMBER: 36,575  
REFERENCE/DOCKET NUMBER: P0958B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8228  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 58 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-566-800A-44

Query Match 3.4%; Score 7; DB 1; Length 58;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 YGGCYGN 104  
Db 35 YGGCYGN 41

RESULT 15  
US-08-566-800A-45  
Sequence 45, Application US/085666800A  
Patent No. 5736364  
GENERAL INFORMATION:  
APPLICANT: Kelley, Robert F.  
APPLICANT: Lazarus, Robert A.  
APPLICANT: Lee, Geoffrey F.  
TITLE OF INVENTION: No. 5736364e1 Factor VIIa Inhibitors  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/566,800A  
FILING DATE: 04-Dec-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kubinec, Jeffrey S.  
REGISTRATION NUMBER: 36,575  
REFERENCE/DOCKET NUMBER: P0958B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8228  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 58 amino acids

TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-566-800A-45  
Query Match 3.4%; Score 7; DB 1; Length 58;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 98 YGGCYGN 104  
Db 35 YGGCYGN 41

Search completed: April 22, 2004, 10:26:18  
Job time : 24 secs